

**GENETIC VARIABILITY AND DIVERGENCE ANALYSIS
IN *JATROPHA CURCAS* L. BASED ON
MORPHOLOGICAL CHARACTERS**

Thesis

SUBMITTED TO THE

**G.B. Pant University of Agriculture & Technology
Pantnagar-263 145 (U.S. Nagar), Uttarakhand, INDIA**



By

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B.Sc. (Agriculture)

***IN PARTIAL FULFILMENT OF THE REQUIREMENTS
FOR THE DEGREE OF***

***Master of Science in Agriculture*
(Genetics and Plant Breeding)**

JUNE, 2016

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ACKNOWLEDGEMENT

In expressing my innate feelings and thoughts, gray matter has brought me at that turning point where my lexicon fails to provide me adequate words to elucidate the deep sense of reverence and indebtedness to Dr. B.B. Bandyopadhyay, Professor, Department of Genetics and Plant Breeding and the Chairman of my Advisory Committee, a dedicated scientist whose inexhaustible power of action, scholastic guidance, constant supervision, wide hearted cooperation, diligence, erudacy and persistent endeavour throughout the period of investigation, all have shaped me in such a way that I become able to construct this manuscript smoothly.

I feel extremely privileged to express my veneration for the eminent members of my advisory committee Dr. M.K. Nautiyal, Professor, Department of Genetics and Plant Breeding and Dr. A.S. Jeena, Professor, Department of Genetics and Plant Breeding for their authentic technical guidance, keen interest and valuable criticism during the course of investigation and preparation of this manuscript.

I am very thankful to Dr. H.S. Chawla, Head, Department of Genetics and Plant Breeding; Dean, College of Agriculture; Dean, Post Graduate Studies, Joint Director M.R.D.C., Librarian University Library, In charge Computer Section, and Dr. N.K. Singh, Professor, Department of Genetics and Plant Breeding, Dr. Usha Pant, JRO, Department of Genetics and Plant Breeding, Mr. Sarawan Kumar ji, Lab Technician (Rice lab in Department of Genetics and Plant breeding), Kalamuddin Bhaiya for providing the necessary facilities for investigation as and when required.

With the deep sense of gratitude and pleasure, I am immensely rejoiced to owe my deep sense of gratitude to Hon'ble Vice-Chancellor, Registrar, and Directors for their sympathetic attitude, timely help and other facilities all along the studies during my M.Sc. programme.

I wish to place on record my appreciation and sincere thanks to Staff members of Department of Genetics and Plant Breeding for their cooperation and support throughout the degree programme.

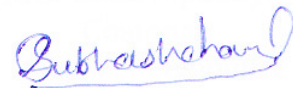
I am very fortunate and lucky to have the ceaseless encouragement and love from my family. The continuous support, moral boost up and blessings of my parents and this is a great time to acknowledge great people, who have always been the torch bearers in the darkest path of life and always be the role models for me and guiding me to. Word would fail to express the depth of my feeling for my Dadi ji, Mummy, Papa, Nana ji, Nani ji, and my dear Uncle and aunty for their blessing, younger sister Hema Kumari and elder sister Shweta Kumari, for providing me with their precious love, care and support.

I would be failing in my duties if, I do not mention the help, guidance and rendered by all my seniors, especially Deepankar sir, Rakesh sir, Jairam sir, Devendra sir, Deepak sir, Anurag sir, Arvind sir, Amarjit sir, lalit sir, Ajay sir, Sanjana mam and Tabassum mam, Anupam sir, and My vocabulary fails to find words to express thanks to my loving juniors Narendra, Ningangouda, Kailash, Tanuj, Tanvi, Vartika and Sanchika.

I am very fortunate and lucky to have the ceaseless encouragement, counsels, pain-taking efforts, support and constructive criticism from my friends and batchmates Ankit, Anil, Deepak, Bharat, Shiv Shankar, Rajeshwar, Akshay, Abdul, Devendra, Himanshu, Gouri Shankar, Sneha, Neha, Neetu, Sonali, Anjana who shared a memorable part of my life. Every moment shared with each of them is a unique feeling to remember.

Lastly, I would also like to thank all who could not find a separate name but have helped me directly or indirectly.

*Pantnagar
June, 2016*



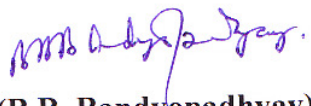
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CERTIFICATE

This is to certify that the thesis entitled “**GENETIC VARIABILITY AND DIVERGENCE ANALYSIS IN *JATROPHA CURCAS* L. BASED ON MORPHOLOGICAL CHARACTERS**” submitted in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE IN AGRICULTURE** with major in **Genetics and Plant Breeding** of the College of Post Graduate Studies, G.B. Pant University of Agriculture and Technology, Pantnagar, is a record of *bona-fide* research carried out by **Mr. Subhash Chand, Id.No. 48105** under my supervision and no part of the thesis has been submitted for any other degree or diploma.

The assistance and help received during the course of this investigation have been duly acknowledged.

Pantnagar
June, 2016


(B.B. Bandyopadhyay)
Chairman
Advisory committee

CERTIFICATE

We, the undersigned, members of the Advisory Committee of **Mr. Subhash Chand. Id. No. 48015**, a candidate for the degree of Master of Science in Agriculture with major in **Genetics and Plant Breeding**, agree that the thesis entitled **“GENETIC VARIABILITY AND DIVERGENCE ANALYSIS IN *JATROPHA CURCAS* L. BASED ON MORPHOLOGICAL CHARACTERS”** may be submitted in partial fulfilment of the requirements for the degree.

(B.B. Bandyopadhyay)
Chairman
Advisory Committee

(M.K. Nautiyal)
Member

(A.S. Jeena)
Member

C O N T E N T S

S. No.	CHAPTER	PAGE NO.
1.	INTRODUCTION	
2.	REVIEW OF LITERATURE	
3.	MATERIALS AND METHODS	
4.	RESULTS AND DISCUSSION	
5.	SUMMARY AND CONCLUSIONS	
	LITERATURE CITED	
	APPENDIX	
	VITA	
	ABSTRACTS	



Introduction



India possesses precious wealth of plant genetic materials. *Jatropha curcas* is one of such an important plant genetic material that could be used for bio-fuel production as an alternative resource of crude petroleum oil used for generating energy for the growth of developed and developing countries in the world. Geopolitical features, increase in hike of crude petroleum oil price and growing demand of fuel in these countries seem to cast a shadow over the supply of crude petroleum oil in many countries including India (Asif and Munee, 2007). The government of India has adopted alternative strategies for the production of biofuels among plants in order to avert the risk of impaired supply of fuels from resource countries.

The genus *Jatropha* of Euphorbiaceae family is one of the potential biodiesel yielding tree crop. It is morphologically a diverse genus comprising 160-175 species of shrubs, rhizomatous shrubs, herbs and small trees. About nine species of *Jatropha* have been reported in India. Among these, important ones are *J. gossypifolia*, *Jatropha curcas*, *J. glandulifera*, *J. multifida* and *J. podagrica*. Out of these species, *Jatropha curcas* is the most important biodiesel yielding crop. It is native of Mexico and South America and grows through-out tropics in the world. The plant is reported to have been introduced in Asia and Africa by Portuguese as an oil yielding plant. In India including Andaman Island, the plant grows in semi wild condition. It thrives well to semi-arid condition, alkalinity /salinity of soil, marginal (Rao *et al.*, 2008) and waste land (Tiwari, 1994) and also in dry environment. *Jatropha curcas* is a multipurpose tree of significant economic importance and commonly known as Rattan-jyot, Chandra-jyot, Jamal-gota, Jangli-arandi, Kala-aranda and physic-nut *etc.* The presence of a toxic substance, ‘curcascine’ makes its oil non-edible. It is a renewable and safe energy source providing a viable alternative option to diesel, kerosene, LPG, furnace oil, coal and fuel wood (Martin and Mayeux, 1985).

The idea of biodiesel was conceived more than 100 years ago when diesel was invented by Mr. Rudolf Diesel and this diesel was made by trans- esterification

process from the vegetable oil and used in a compression ignition engine. Because of the high cost involved in the production of diesel from vegetable oil, mineral diesel replaced it as a source of combustion fuel. Owing to the well-established advantages of biodiesel, its production has witnessed a double digit annual growth rate for the last few years worldwide. Major sources of biodiesel include sunflower (Italy and Southern France), rapeseed (USA), soybean (USA and Canada), beef tallow (Ireland), cottonseed (Greece), and jatropha (Nicagua and South America) (**Jaisingh, 2004**). Among the potential candidate crops, *J. curcas* has attracted the interest of various developmental agencies in the tropics and subtropics not only due to its easy adaptability to semi-arid marginal sites, but also for its oil as diesel fuel substitute and exploitation of waste-land.

Biodiesel is expanding very fast because of demand, policy support and technological availability. Globally the oil provides energy for 95% of transportation and the demand of transport fuel continuing to rise every year. According to inter-governmental panel on climate change (IPCC), global oil demand will rise by about 1.6% from 75 million barrel per day in the year 2000 to 120 million barrel per day by 2030 (**Anonymous, 2003**). It seems that the transport sector alone will constitute at least 75 per cent of the increased demand as oil will remain the fuel of choice in all forms of transportation viz., road, sea and air.

Bio-diesel is considered as clean fuel because the absence of sulphur, aromatic compounds and presence of about 10 per cent built in oxygen helps it to burn fully. The combustion of biodiesel improves considerably due to its higher cetane number (51) even when blended in the petroleum diesel (**Anonymous, 2003**). Amongst the biofuels, ethanol and biodiesel are gaining world-wide acceptance as a solution for socio-economic and ecological problems such as environmental degradation, restricting imports, energy security, rural employment and agricultural economy. Ethanol is used as fuel or as oxygenate to gasoline. Raw material used for producing ethanol varies from country to country such as sugar in Brazil, cereals in USA, sugar-beet in Europe and molasses in India. Ethanol is used as 100% fuel in about 20% of vehicles and 25% blend with gasoline in the rest of vehicles in Brazil. USA uses 10% ethanol gasoline blends, Australia uses 10% ethanol- gasoline blend and 5% blend in Sweden. Use of 5% ethanol- gasoline blend is already approved in some states of

India but Bureau of Indian Standards (BIS) is planning to implement this in the whole country. BIS standard for 10% blends need to be drafted after conducting trials and fixing parameters. As bio-diesel has properties similar to petroleum diesel fuel, there is no need for modification in the design of engine using up to 20 % blend however, minor modification are required for higher percentage blends.

Since the oil crisis of the 1970s and recognition of the limitation of world resources, jatropha has received attention of the researchers and policy makers to meet the domestic need from natural resources. Government of India launched ---- National Mission on Bio-diesel with a view to find a cheap and renewable liquid fuel based on vegetable oil (**Shukla, 2005**). In India, the maximum jatropha cultivation is being done in the state of Chhattisgarh followed by Maharashtra, Gujarat, Tamil Nadu and Rajasthan. The cultivation of jatropha at present is not economical under agriculture system due to non-availability of high yielding varieties, deterioration of seed quality under ambient storage conditions and several biotic and abiotic factors. Necessary improvement thus requires establishing jatropha as a remunerative crop among the farming community.

The physic nut is a small tree or large shrub which can grow up to 5 m. Inflorescences are complex branched cyme and located terminally on each branches. The plant is mostly monoecious and flowers are unisexual; occasionally hermaphrodite flowers occur. In the androecium, ten stamens are arranged in two distinct whorls of each in a single column in close proximity to each other. In the gynoecium, the three slender styles are congenitally joined to about two-thirds of their length; expanding into massive bifurcate stigmata (**Dehgan and Webster, 1979**). Pollination of physic-nut is by insect. The pistillate flowers open earlier than staminate flowers in the same inflorescence *i.e.* protogynous in nature (**Heller, 1996**).

Jatropha is derived from Greek word, *Jatros* = Doctor and *Tropha* = Nutrition (**Sahu et al., 2008**). It has multi-purpose utility like (i) the plant exude which is sticky, bitterly pungent and astringent latex, can be used as making ink; (ii) the bark contains tannin, wax, resin, saponins etc., which makes it useful for industrial purposes and (iii) medicinal importance which is used for curing health of human being and animals *viz.*, antidote for snake bites, leprosy and rheumatism, treatment of tooth ache and muscular pains, pile, fever, jaundice, gonorrhoea, constipation, heart burn, anti-

malarial, insecticidal, anti-cancerous and anti-tumour properties. The chromosome number of *Jatropha curcas* was found to be $2n=22$ (Perry, 1943 and Sarkar, 1989). It grows between 4 to 5 m height and has large green to pale-green deciduous leaves with several yellowish flowers and 2.5 to 4 cm long bell-shaped green capsules (fruits), which turn yellow when ripe (Morton, 1977). The species is adaptable to a wide range of soils and climates (up to 500 m above mean sea level; mean annual temperature ranging from 20 to 28°C with mean annual rainfall of between 100 to 2000 mm) and grows well without any special nutrition regime (Patil and Singh, 1991 and Beentje, 1994). Because of its lower water demands, low soil fertility requirements and tolerance to high temperature stress, it can grow well under any unfavourable agro-climatic conditions (Diwaker, 1993 and Tiwari *et al.*, 1994). The species is highly cross pollinated and can be propagated either from seeds or by vegetative propagation through cuttings of stem or branch. Flowering and fruiting commence one year after planting, but economic yield achieves after three years and produces large quantity of seeds over a period of 50 years (Aker, 1997). *Jatropha* seed contains considerable amount of protein (18.00%), fat(38.00%), carbohydrates (17.00%), fibre (15.00%), and ash (5.30%).The seeds of *jatropha* contain 46 to 58% of oil on kernel weight and 30 to 40% on seed weight basis (Subramanian *et al.*, 2009). The oil is a rich source of hydrocarbon (27 to 48.5% of seed oil) hence, it has gained importance as a potential biofuel crop (Umamaheswari *et al.*, 2010).The oil/fat contains about 21% saturated fatty acids and 79% unsaturated fatty-acid (Raja *et al.*, 2011).

The oil is used for illumination without smoke, substitute of diesel, kerosene, lubricants, soaps and candle manufacturing. It can be used as hair oil and has application to live-stock against sores. As an excellent source of organic manure, it contains 1.2% potash, 1.4% phosphorus and 3.2% nitrogen (National Oilseeds and Vegetable Oils Development Board; Ministry of Agriculture, Govt. of India, 2007-08).

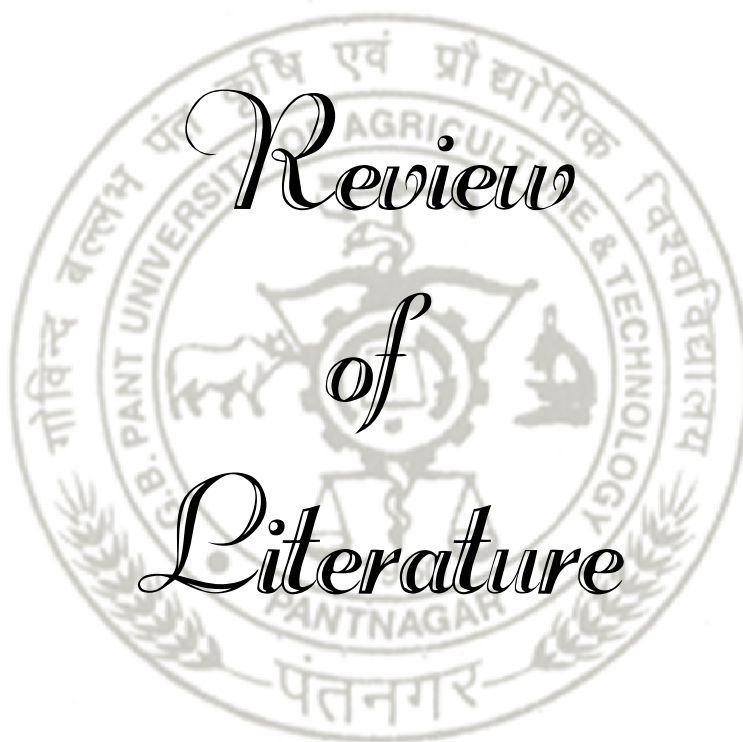
The development of Indian economy is directly and proportionately rests on commensurate increase in energy demand and rising oil imports. Ministry of Petroleum and Natural Gas (2009) mandates the use of 5% ethanol blending of petrol, initially for selected states and union territories, and later extended to the

whole country. It is also initiated a programs for stimulating complementary use of biodiesel to displace petroleum based diesel and also emphasize the production of biodiesel preferably from non-edible oil seeds of different crops mostly grown over marginal or degraded lands. The Government of India approved the National Policy on Biofuels in year 2009 targeting a 20% blend of biofuels with gasoline and diesel by 2017.

Jatropha species are essentially cross pollinated, which offer a high degree of variation and provide ample scope for screening and selection of seeds from suitable sources of the desired traits (**Ginwal *et al.*, 2005**). Since variability is a pre-requisite for selection programme and the tremendous variability for oil content (28-40%) in seeds of *Jatropha curcas* accessions from different agro-climatic regions of India have been reported (**Ginwal *et al.*, 2005** and **Kaushik *et al.*, 2007**). It is necessary to detect and document the amount of variation existing within and between the populations of *Jatropha curcas* for its genotypic improvement in terms of altering its status from wild perennial form to a cultivable crop with higher seed yield and seed oil content. Little is known about the genetics, breeding, physiology and agronomic aspects of the species. Different breeding programs for *J. curcas* have been implemented in Brazil (**Achten *et al.*, 2010**). The use of efficient methods of improvement depends fundamentally on the knowledge regarding the genetic control of the traits to be improved, genetic divergence, gene actions, heritability, correlation between traits and its interaction with environment at growing site (**Hallauer, 2007**). In this present investigation emphasis is given to study “Genetic variability and divergence analysis in *Jatropha curcas* L. based on morphological characters”.

Considering the importance of *Jatropha curcas* and its multiple utility, the present study was designed in priority with following objectives:

1. To estimate relative morphological variability and genetic divergence among *jatropha* genotypes for different characters.
2. To determine heritability (h^2) and genetic advance (GA) for various agronomic characters.



*Review
of
Literature*



In this chapter an attempt has been made to review the relevant literature on different aspects of the *Jatropha curcas* under following headings.

2.1 Botany

2.2 Genetic variability, Heritability and Genetic advance

2.3 Genetic divergence

2.1 Botany

Wanchali *et al.* (1986) studied floral biology and fruiting setting of *J. curcas*. They described inflorescence as a compound dichasial type. Anthesis begins after 17 days after flowering and the pollination starts 9-10 am. Pollen grains are sub-spheroidal in form. The pollen viability was 92% but germination was only 22.5%. The growth and development of fruit after pollination took 45 days. Fruit is classified as nut with 3 locules and taper in shape.

According to **Solomon and Ezradanam *et al.* (2002)** *Jatropha* is a monoecious, protandrous and subtropical shrub. They observed 27:1 ratio of male to female flowers. The sexual system facilitates geitonogamy and xenogamy. *Jatropha* is an entomophilous plant and pollination is aided by ants, bees, flies and thrips. Geitonogamy and xenogamy is affected by bees and flies, while ants and thrips affect only geitonogamy. Self-pollination through geitonogamy is thought to be adaptive process for *Jatropha curcas* for colonization.

Bhattacharya *et al.* (2005) attributed that male flower produced 1617 ± 100 pollen and the ration between pollen: ovule was 539:1. The stigma became receptive at 2hr after flowering. Female flower produced higher amount ($4.54 \pm 0.82\mu$ litre) of nectar than male flowers ($1.92 \pm 0.44 \mu$ litre). Nearly 50% of female flowers set fruit with 2:3 ratio between seed and ovule seed. The plant also exhibited 32% apomixes. The flowers attracted hymenopteran (*Apis* spp.) and coleopteran pollinators. Among the different insect visitors, *Apis* spp. was the most frequent.

Li et al. (2007) studied pollen-ovule ratio (P/O) and pollen viability on *Jatropha curcas* in Yuanjiang Country, Yunnan Province. They concluded that it had unisexual flower with dichasial inflorescence. The life span of male and female flowers was about 2 days and 12 days, respectively. The diameter of female flower was bigger than that of the male flower slightly. The pollen viability reached high in 9 hours after blooming and decline to low 33 hour later. The stigmatic receptivity of female flower was strong during 1st to 4th day. Stigma completely lost its receptivity on the 9th day. The effective pollination way of *Jatropha curcas* was carried through insect pollination and exhibited self-compatible mode of reproduction as well.

Yang et al. (2007) studied on pollination biology, fruit set and seed production of *J. curcas*. They observed that a total of 17 species of insects visit the flower out of which 11 of them were pollinators. *Apis mellifera* and *A. cerana* were the most effective pollinators due to their highest visiting frequencies. The pollen activities of the flower had 5-6 days. The fruit sets of artificial self-pollination, artificial cross-pollination and natural pollination were reported 87.93, 86.66 and 76.42%, respectively, which indicated that artificial induction of hybridization become feasible for effective fruit setting.

Malaipan et al. (2008) observed the variation of pollen germination. They reported that pollens were collected from florets at the apex of inflorescence (68%) had better germination than those pollen collected from the middle (64%) or at the base (58%) of inflorescence. Per cent germination of the late blooming inflorescence (74%) was higher than that of early blooming inflorescence (54%). Pollen from the florets at the first group blooming on the stem (55%) had lower germination than the second (77%) or the third (75%) group. Sex ratio of female and male flowers (1:9) was higher in March and decreased (1:22) in October. Insect pollinators preferred visiting on female flowers (21%) less than male flowers (31%) in March, but in October, they visited female flowers (2.2-3%) more than female flowers (1.7-2%).

Pranesh et al. (2010) observed cross pollinated mode of reproduction in *Jatropha curcas* at UAS, Bengaluru. The plant produces dichasial inflorescences with unisexual flower. Male and female flowers were produced in the same inflorescence. The less numbers of male flowers were produced than female flowers in the same inflorescence. Pollination between different flowers from the same or different plants

only led to the development of fruits and the ratio between male to female flower was around 14.4 to 105.73. *Jatropha curcas* however facilitate sexual system of geitonogamy and achieved success in fruit setting up to 75.6%. While out-crossing yielded up to 74.97 per cent of fruit set. They observed a tendency to promote xenogamy and minimize geitonogamy through differential opening of male and female flowers.

Luo *et al.* (2011) studied behaviour of diurnal and nocturnal insects on pollination. They reported that both nocturnal and diurnal visitors were successful pollinators. Flower received significantly more visits by diurnal insects than by nocturnal insects and contributes more to seed production of *J. curcas*. Nectar production of both male and female flowers attained high in the morning, declined in the afternoon, and rapidly reached at bottom end during the night in all of their anthesis days.

Ramirez *et al.* (2013) observed terminally or axillary developed solitary inflorescences which varied in length from 5 to 25 cm. They were mostly bisexual, however, unisexual flowers also observed. Bracts present on the inflorescences were lanceolate without marginal glands, 2–15 mm in length, and their distal axes were purulent. The percentages of male (8.6%) and female flowers (10 to 20%) in inflorescence varied from plant to plant, and population to population, in response to prevailing environmental conditions.

Negussie *et al.* (2014) studied the effect of different pollination methods on fruit and seed yield at two locations in Zambia and Malawi. Autogamous pollination led to fewer fruit set and low seed yield at Zambia sites, whereas, more mature fruits but with fewer seeds were obtained in Malawi. Furthermore, high fruit and seed yield was recorded in case of open pollination as well as in pollen supplemented pollination at Zambia sites indicating pollen abundance at this site. On the other hand there was no seed yield difference between pollination treatments at the Malawi site. The seeds production is encouraged by both self-and cross-pollination and those factors that promote natural pollination.

Silvia *et al.* (2014) evaluated 17 *Jatropha* accessions for their flower characteristics; mode of reproduction, fruit set, fruit fresh weight, number of seeds per

fruit, seed dry weight, and oil content. They observed high fruit set (64 %) through apomixes than natural pollination (10.1%) and relative performance of fruit fresh weight, number of seeds per fruit, seed dry weight, and oil content were influenced by mode of reproduction.

2.2 Genetic variability, Heritability and Genetic advance

Ginwal *et al.* (2004) studied *Jatropha curcas* seed sources collected from ten locations representing the states Madhya Pradesh and Maharashtra and observed significant differences among them for height, collar diameter, number of branches, leaf area and field survival. Seeds collected from different sources also varied significantly in respect of seed and kernel weight and oil content in seed/kernel. The study of genetic parameters revealed the significant positive correlation of growth traits with each other. Fair differences between phenotypic and genotypic coefficient of variability were observed. Heritability (broad sense) values were fairly good with regard to leaf area, height and collar diameter in comparison to survival per cent.

Rao *et al.* (2007) studied genetic association and variability in seed and growth characters in 32 high yielding genotypes of *Jatropha curcas* collected from different locations. Estimates of broad sense heritability were found to be high exceeded 80% for all the seed traits. Female to male flower ratio showed near to 100% heritability followed by yield (83.61) and plant height (87.73).

Gohil *et al.* (2009) evaluated nine genotypes of *Jatropha curcas* L. in terms of the amount of variability, GCV, PCV, heritability, genetic advance and genetic gain for 14 characters. All the genotypes differed significantly for most of the characters except primary branches. The estimates of phenotypic coefficients of variation were found higher for plant height, plant canopy, collar diameter, number of primary and secondary branches, average seed weight, number of seeds and capsules, number of leaves, seed yield and oil content. Whereas higher GCV estimates were observed for the traits like seed yield, plant canopy, number of leaves, seed oil and kernel oil had. Study concludes that plant canopy, seed yield and number of leaves, seed oil and kernel oil content showed high heritability coupled with high genetic advance. So emphasis could be given on these parameters during selection to improve *Jatropha* varieties/genotypes.

Das et al. (2010) reported moderate to high heritability along with high genetic advance for seed yield per plant, fruits per plant and flowering bunches per plant in an experiment on sixteen *Jatropha curcas* genotypes collected from four states in India. The results indicated preponderance of additive gene action and selection for these characters would be effective.

Freitas et al. (2010) evaluated 75 *J. curcas* progenies collected from Brazil and three from Cambodia with an objective to quantify genetic diversity and to estimate genetic parameters for growth and production traits and seed oil content. The mean oil content in the seeds was 31%, ranging from 16 to 45%. No genetic correlation between growth traits and seed oil content was found. High coefficients of genetic variation were found for plant height, number of branches, height of branches and stem diameter. The highest individual narrow-sense heritability was found for leaf length (0.35) and width (0.34), stem diameter (0.24) and height of branches (0.21).

Gairola et al. (2011) suggested that variability studies are the prerequisite and of paramount importance for developing tree improvement strategy. Naturalized stands of *Jatropha curcas* spread all over India and due to varied climatic conditions across the country are likely to have a high degree of variability. The variability in seed characteristics was analysed in this investigation. Significant differences were found among the seed sources for all the parameters. The mean fruit weight ranged from 2.21 to 3.41g, seed weight from 0.58 to 0.81g, seed length from 1.49 to 1.81cm, seed circumference from 2.97 to 3.51cm, seed moisture content from 6.20 to 10.44% and seed germination from 53.33 to 79.83%. The genetic component analysis revealed that heritability value was found high for seed germination percentage (85.34%) coupled with moderate genetic gain which signifies that seed germination is under genetic control can be used for improvement of this species.

Shabanimofrad et al. (2011) conducted an experiment to determine the genetic components and relationship among physic-nut genotypes in Malaysia. They used fourteen morphological characters. Analysis of variation revealed significant difference for all the characters among genotypes. Oil yield per ha had maximum phenotypic coefficient of variation followed by total number of seeds/ plant and seed yield/plant. Similarly, seed yield/plant had maximum genotypic coefficient of variation followed by oil yield/ ha and total number of seeds/ plant. More than 63.5%

of broad sense heritability was found for all the characters. Seed yield and total number of seeds/ plant had higher value of genetic advance (>70%). High GCV, heritability and genetic advance was found for primary branches/plant, total no. seeds/plant, total branches/plant and seed yield/plant. Seed yield showed significant difference and positive correlation with total no. of seeds, total branches, leaf greenish, plant height, number of fruits and oil yield.

Rafii *et al.* (2012) conducted an experiment to evaluate six physic-nut genotypes in Malaysia. Genetic variability, heritability and inter character association of seed yield and other component traits were study. The experiment was conducted in Randomized Complete Block Design with three replications, six genotypes per replication and sixteen plants per plot. ANOVA showed highly significant variation for total seeds/genotype, seed thickness, plant height, seed breadth. The maximum broad sense heritability was observed for plant height (23.04%). On the basis of experiment it can be concluded that environment had a great role than genetic factors. The seed length had significant and positive correlation with seed weight, seed breadth and seed thickness. Thus genotypes V2 and V5 are superior parents which can be used in *Jatropha* breeding programme for development of high seed yielding cultivars.

Guan *et al.* (2013) conducted an experiment to study the characterization of seed morphology and genetic diversity of *Jatropha curcas* L. from eight different provenances. The genetic diversity of eight populations from different provenances was estimated using DALP method (5 primers). The results showed that seed morphology had significant variation among locations. Five DALP primers generated highly reproducible and stable DNA fragments. 219 of 244 loci were polymorphic, i.e., PPB was 89.75%. And POPGENE analysis indicated the total Nei's gene diversity (H) was 0.2878, the total Shannon's Information index (I) was 0.4331, and the coefficient of Gene differentiation (Gst) was 0.8200 among populations, namely 82.00% genetic variation occurring among populations and 20.00% remaining within population.. The high genetic variability was found in *Jatropha* population not only through genetic drift but also through limited gene flow. The result indicates that the seed morphology among populations showed some kind differentiation. The 8 populations show high level of genetic diversity and genetic differentiation. So that selection based on regional basis should has great potentiality.

Sharma *et al.* (2013) conducted an experiment to assess genetic components in *Jatropha* crop. Data were obtained on 10 morphological traits during year 2007 to 2008 and 2008 to 2009. High estimates of heritability (h^2) coupled with high genetic gains (GA) were registered for number of fruit clusters/plant, seed yield/plant and dry fruit yield/plant for both years which implies that direct selection would be effective for improvement of these traits.

Brasileiro *et al.* (2013) studied the genetic parameters among twenty half sib family of *Jatropha* population. The use of efficient breeding methods depends on knowledge of genetic control of traits to be improved. The mean progeny heritability values were: 50% for number of bunches, 47% for number of fruits, 35% for number of seeds, 6% for stem diameter, 26% for number of primary branches, 14% for number of secondary branches, 66% for plant height, and 25% for survival of the plants, demonstrating good potential for early selection in plant height, number of branches, and number of fruits per plant. It demonstrated the possibility of obtaining genetic gains for yield contributing characters.

Tripathi *et al.* (2013) examined 113 *Jatropha curcas* clonal accessions collected from different regions of India. High heritability was observed for fruits per plant, seeds per plant, 100-seed weight, seed/kernel (S/K) ratio and kernel oil percentage coupled with high genetic advance suggesting that the accessions can be considered improvement. The significant positive association of seed oil content (%) with 100-seed weight suggested the effectiveness of indirect selection for seed oil content through 100-seed weight. Five Accessions viz., 76, 120, 29, 86 and 84 were identified as the best genotype and could be selected as parents' for further improvement.

Sharma *et al.* (2013) conducted studied on *Jatropha* to determine the variation in fruit and seed characteristics. The range, mean, phenotypic and genotypic coefficient of variability, heritability, genetic advance and genetic gain was estimated. Significant variations were recorded in all characters. High heritability in seed length (79.04%), fruit length (66.61%), fruit width (66.33%) and seed weight (47.55%) there is scope for considerable genetic gain through individual plant selection. On average *Jatropha* plant selections namely HP-31 and HP-35 were found to be better on the basis of fruit and seed morphological characteristics.

Shabanimofrada *et al.* (2013) examined the genetic variation and relationship among forty-eight physic-nut genotypes in Malaysia by using fourteen morphological characters. ANOVA showed highly significant differences for all the genotypes. The maximum phenotypic coefficient of variation was found for oil yield/ ha followed by seed/ plant and seed yield. The maximum genotypic coefficient of variation was found seed yield followed by oil yield / ha and total number of seeds per plant. Broad sense heritability was found more than 63.5% for all the studied characters. The genetic advance was observed higher for seed/ plant and seed yield. Morphological traits viz. total number of branches per plant, total number of seeds per plant, seed yields per ha and number of primary branches per plant exhibited a high GCV, heritability and genetic advance. Seed yield showed positive correlation with number of fruits plant height, leaf greenish, total number of seeds, total branches and oil yield.

Genetic association and variability were studied by **Singh *et al.* (2013)** in twenty genotypes of physic-nut for seed and oil yield contributing characters. Genotypic variance was lower than phenotypic variance for all traits. High heritability coupled with higher genetic advance was found for plant height (74.101%, 80.171), oil content (77.956%, 16.210) and fruit set (57.430%, 15.890). Sufficient amount of genetic variability was noticed among the physic-nut genotypes.

Bochalya *et al.* (2015) studied the variability and character association for oil content and 26 characters of *Jatropha*. The experiment was conducted on 3 and 4 year old *Jatropha* plants during 2007-08. Analysis of variance revealed significant differences among the genotypes for all the traits except for number of primary branches per plant in both the years. Correlation of oil content with plant height, stem girth, number of fruits per fruiting branch, petiole length, number of secondary branches per plant, weight per fruit, 100-seed weight, seed yield per plant, seed content and kernel: shell ratio was significant positive in both the years. The positively correlated characters which exhibited positive direct effects on oil content were seed content, number of fruits per fruiting branch, weight per fruit and kernel: shell ratio at both the ages. Significant inter correlations were also existed among the characters associated with oil content.

Kumar *et al.* (2015) performed a study on intra-specific crosses of physic-nut. These crosses were developed by using 10 parents to evaluate genetic variability, broad sense heritability, genetic advance and genetic advance over the mean for plant growth and seed yield contributing characters. ANOVA showed that that all the crosses were significantly different for growth and seed yield contributing characters. The hundred seed weight ranged from 49.8 g (NRCJ-35) to 61 g (NRCJs-26). Seed yield per plant showed maximum and minimum mean values for NRCJ-15 (733 g) and NRCJ-30 (177.5 g). The phenotypic and genotypic coefficient of variation of hundred seed weight was 10.93 and 3.37, respectively whereas genetic advance as per cent of mean (3.37%) and heritability (30.86) was moderate. The phenotypic and genotypic coefficient of variation of seed yield was 21.61 and 8.42, along with moderate heritability (38.96 %) and genetic advance (65.81 %). The study revealed that the variation found in different characters can be effectively utilized in genetic improvement of the species and good performing crosses can be utilized for large plantation under biofuel development programme.

Kaushik *et al.* (2015) conducted an experiment in sandy loam soils poor in organic carbon and water holding capacity in southern Haryana, India to determine the best progenies of *Jatropha curcas* for bio-diesel production. Fifty progenies raised from seed sources collected from nine different states of India and were evaluated after five years of plantation for growth, seed yield and oil content contributing characters. The progenies showed significant ($P > 0.05$) differences for all the traits studied. Maximum seed yield per plant (879.37 g), capsules/plant (522.67) and plant height (408.33 cm) was recorded in P-44. Maximum oil content observed in P-37 (36.08%) followed by P-5 (35.64%). The magnitude of phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) for all the characters studied. Heritability was highest for oil content (95.49%) and 100-seed weight (87.75%) followed by seed yield (75.54%). Total capsules/plant exhibited highest genetic advance (92.69%) followed by number of branches per plant (64.32%).

Freitas *et al.* (2016) described *Jatropha* as a potential biodiesel producing crop, but very less amount of genetic studies and breeding programmes were conducted on this crop. Genetic components were estimated on ten yield contributing

characters among seventy-seven half-sib progenies of physic-nut after fifty-two months (from planting of the seeds) in the field. They evaluated correlations between yield contributing characters and the oil content of the seeds. The general mean of grain yield/ plant was 377.9 g and for oil content it was 36.2%. Moderate level of heritability was found for fruit length, seed width, seed length and grain yield/plant. Oil content showed significant and positive correlation with hundred seed weight.

2.3 Genetic divergence

Genetic divergence is basic requirement and criteria for choosing the parents for recombination and breeding programmes. Sufficient genetic diversity is necessary to be present in the base population for the selection of genotypes as potential parents in hybridization programme. The more diverse parents more will be the chances of increased spectrum of variability and greater will be the opportunity for obtaining superior combination of gene in genotype with desire traits. Different classical approaches based on multivariate analysis are available. Mahalanobis's D^2 statistics (Mahalanobis, 1936), clustering by Tocher's method (Rao, 1952) a non hierarchical cluster analysis (Beale, 1969) and elaborated by (Spark, 1973), conical analysis (Anderson, 1958), metro-glyph analysis (Anderson, 1957) are some of the multivariate analysis method used to classify the genotypes into different groups and for effective utilization in plant breeding and in cultivar improvement programme.

Very few literatures are available to describe the genetic divergence in *Jatropha* population. Some of them are presented below:

Rao *et al.* (2007) performed genetic diversity analysis in *Jatropha* genotypes and described hierarchical clustering by Ward's minimum variance. Cluster analysis revealed phylo-geographic patterns of genetic diversity. K-means clustering showed that *Jatropha* genotypes from different eco-geographic regions were grouped together in a single cluster, whereas the genotypes which were collected from same eco-geographic regions grouped into different clusters. It suggested that geographical diversity may not be related to genetic diversity.

Gohil and Pandya (2008) grouped the *Jatropha* genotypes into five clusters by applying Mahalanobis D^2 statistics. Two genotypes were found in Cluster I and III; three genotypes were found in cluster II and single genotype was found in cluster VI

and V. The maximum intra cluster distance was obtained for cluster II. So these genotypes had maximum divergence. The maximum divergence was found between clusters I and cluster V; minimum divergence was found between cluster V and cluster VI. In general, cluster III and IV showed high and low mean values for most of the characters.

D^2 statistics was used in *Jatropha* by **Rao *et al.* (2009)** to estimate the genetic diversity in the population. Results indicated substantial variability for most of the traits. The wide range of D^2 values and segregations of accessions in to as many as 12 clusters is a clear evidence for high degree of genetic divergence among *Jatropha* accessions. Ten out of twelve characters contained one to four accession indicating their unlikeness and substantial genetic divergence among them.

Mahalanobis D^2 analysis grouped forty genotypes in to eight clusters. Cluster VI had seven genotypes. Cluster I and IV had equal number of genotypes (six). Cluster III had only single genotype. Intra-cluster distance was found maximum for cluster VIII (50423) followed by cluster IV (4.131), V (4.085), I (3.915) and cluster II (3.831). Inter- cluster distance was found Maximum between cluster III and VIII (9.922) followed by between cluster V and VIII (8.085). On the basis of high cluster mean and wide genetic distance, the superior genotypes of cluster III (PT-19) and cluster V (PT-24, PT-8 and PT-18) may be used as potential parents for *Jatropha* improvement programme (**Hooda *et al.*, 2009**).

Freitas *et al.* (2010) used a clustering algorithm and concluded that geographical diversity did not necessarily represent the genetic diversity among the accessions collected. These results are important for the continuity of breeding programs, aimed at obtaining cultivars with high grain yield and high oil content in seeds.

In *Jatropha*, **Mahmoodreza *et al.* (2011)** assessed genetic diversity using multivariate analysis and on the basis of the six quantitative characters viz.; seed length, seed width, fruit length, fruit width, 100 seed weight and oil content, grouped the fifteen nine accessions into three clusters at a coefficient level of 3.7.

Sharma *et al.* (2013) assessed the genetic diversity and magnitude of association of different characters in a set of 35 diverse genotypes of *Jatropha*. All the

component traits showed positive and significant correlation with fruit weight except for the number of productive branches which showed negative correlation. Maximum contributions toward total divergence were observed in case of plant height, fruit size, length, number of fruits per plant and fruit weight per plant. The highest number of genotypes appeared in cluster III with 17 entries followed by cluster I and cluster II with 9 and 5 genotypes, respectively, whereas clusters IV, V, VI and VII had 1 genotype each. The highest intra-cluster distance was observed in cluster III, while, the lowest intra-cluster distance was noted in clusters IV, V, VI and VII. It is suggested that for varietal improvement, selection followed by hybridization among the genotypes will be a suitable approach for better exploitation of heterosis in *Jatropha*.

Ramanuj *et al.* (2013) studied genetic variability of eighty *Jatropha* genotypes. They reported that oil content had a range from 20.8 to 36.1%. Thirty seven genotypes revealed high mean values for seed weight/plant (180.2g) while 26 accessions showed high oil content (26.2%). Four clusters were formed by hierarchical cluster analysis from all the genotypes. Clustering patterns revealed that majority of genotypes were genetically similar to each other and grouped in to clusters II. The intra cluster distance was found maximum (30.15) for cluster IV. The inter cluster distance was found minimum (47.59) between cluster I and cluster II and maximum (211.27) between cluster III and cluster I. Maximum genetic distance was found between clusters I and III, followed by cluster I and IV suggesting comparatively wider genetic diversity existed among them. The Principal Component Analysis (PCA) showed that first four principal components (PCs) accounted for more than 93% of the total variation. The first principal components accounted for 42.5% of the total variation mainly due to seed width, seed length number of seeds/plant and seed weight/plant, which had maximum and positive weight on this component.

Guan *et al.* (2013) conducted an experiment to study the genetic diversity and the characterization of seed morphology of *Jatropha* from eight different regions. The genetic diversity of 8 populations from different locations was estimated using DALP method (5 primers). The results revealed that seed morphology had significant variation among different regions. Five DALP primers generated highly stable and

reproducible DNA fragments. 219 of 244 loci were polymorphic, i.e., PPB was 89.75%. And POPGENE analysis indicated the total Nei's gene diversity (H) was 0.2878, the total Shannon's Information index (I) was 0.4331, and the coefficient of Gene differentiation (G_{st}) was 0.8200 among populations, namely 82.00% genetic variation occurring among populations and 20.00% remaining within population. It was suggested that a high level of genetic variation should be occur among the different populations of *Jatropha*. The high genetic differentiation among the populations emerged not only the through limited gene flow ($N_m = 0.1097$) but also through the genetic drift. The result revealed that the seed morphology among populations showed some certain differentiation. The 8 populations had high level of genetic diversity and show apparent genetic differentiation. So that regional selection has great potentiality.

Brasileiro *et al.* (2013) studied the genetic diversity among twenty half sib family of *Jatropha* population. In the analysis of genetic diversity, genotypes were divided into 4 groups. Genotypes 18, 19, 20, and 8 clustered together and presented the highest means for the yield and other yield associated traits.

Shabanimofrada *et al.* (2013) examined the genetic diversity among 48 *Jatropha* genotypes. They studied fourteen morphological characters during 2009–2010 in Malaysia. Based on principal component analyses and UPGMA cluster analysis, genotypes viz., D-01-09 and B-03-02 were grouped into a single cluster. These genotypes were found superior to over other genotypes with respect to total number of seeds, seed yield, number of fruits, primary branch, leaf greenish, oil yield and plant height. These two genotypes can be used as parents in the *Jatropha* crop improvement programme and these genotypes could be hybridized with the genotypes (B-02-01, B-02-05, B-02-04 and B-01-07 and B-05-05) of distant clusters I and II.

Genetic parameters and divergence were studied by **Singh *et al.* (2013)** in twenty four *Jatropha* genotypes for seed and other related traits. Based on D^2 analysis, twenty genotypes were partitioned into fourteen clusters. cluster XI had three genotypes (BRS-03/06-WbB, BRS-12/05-UpA2 and BRS-12/05-UpA3), clusters I, III, V, IX, XIV had only one genotype in each case and clusters II, IV, VI, VII, VIII, X, XII and XIII consisted two genotypes. The range of Intra-cluster distance was found from 0.00 to 12.220 and the range of Intra-cluster distance was found from

7.868 to 70.340. Cluster XIV and VI had maximum inter-cluster distance. Hence, they were the more genetically diverse and could be utilized in *Jatropha* hybridization programme.

Sharma *et al.* (2013) conducted an experiment in *Jatropha* on ten biometric traits during 2007-08 and 2008-09. Non-hierarchical Euclidean analysis showed maximum Euclidean distance between Sowar and IGAU Raipur (11.21%). This analysis partitioned 46 *Jatropha* lines into five different clusters. Cluster I and IV showed maximum inter-cluster distance (7.723), while cluster I and IV showed minimum inter-cluster distances (2.747). A pooled clusters were performed based on three method of cluster analysis viz., metro-glyph clustering, non-hierarchical clustering and hierarchical clustering. The pooled cluster analysis was found effective for the selection of superior genotypes. These genotypes can be used as a donor parent in *Jatropha* crop improvement programme.

Rao *et al.* (2015) performed an experiment on 10 elite genotypes of *Jatropha* for three years at CRIDA, Hyderabad. ANOVA showed that all characters had significant variation among genotypes. Genotype $\times$ environment interaction also appeared significant for all traits. The broad sense heritability was found higher for all characters which indicate that all these characters were controlled by genetic factors. ANOVA suggested that environment also have a great role for the expression of traits. Seed yield/ plant showed positively correlation with pod weight, oil yield and pods/ plant. Based on D^2 analysis genotypes were grouped into three clusters. Cluster I had five genotypes, cluster II consisted only single genotype and cluster III had four genotypes. The high genetic variation between *Jatropha* genotypes showed that these genotypes can be used as a donor parents in *Jatropha* crop improvement programme

Kaushiket *al.* (2015) studied hierarchical euclidean analysis among fifty progenies of *Jatropha* using D^2 statistics. They observed D^2 analysis grouped the progenies into five clusters. The intra cluster distances ranged from 1.33 to 2.72. The maximum inter-cluster distance was observed between cluster II and V (6.43) followed by I and V indicating greater divergence among progenies belonging to these clusters and an attempt to cross the progenies in these clusters should bring out desirable gene combinations and aids in selecting the improved varieties.

Joshi and Nautiyal (2015) conducted a trial to evaluate genetic diversity on forty-six accessions which were collected from different regions of India. On the basis of D^2 analysis, accessions were partitioned into 8 clusters. Single accession was found in cluster I, IV, V, VI; twenty four accessions in cluster II, nine accessions in cluster III, seven in cluster VII and two accessions in cluster VIII. Maximum intra-cluster distance was found in cluster II followed by cluster VI. The maximum inter-cluster distance was found between cluster I and VIII. For all the characters, cluster I and IV showed high and low mean values, respectively. Thus parents should be selected from diverse clusters to obtain high seed yield cultivars and to create more diversity in segregating population.



*Materials
and
Methods*



The present research work was undertaken at Medicinal Plant Research and Development Centre (M.R.D.C.) of G.B. Pant University of Agriculture and Technology, Pantnagar during 20015-16 and investigation was done on twenty genotypes. Pantnagar is geographically situated at 29⁰N latitude, 79.3⁰E longitude and at an altitude of 243.84 m above mean sea level. It falls under humid sub-tropical climate zone and is located at the foot-hills of the Shivalik range of the Himalayas in a narrow belt called *Tarai*. The soil is rich in organic matter with heavy texture.

3.1 Experimental material

The genotypes were planted during 2005 under the Project of National Network of Integrated Development of Tree borne oil seeds and present study was conducted during the year 2015-16. The age of plants in July, 2015 were 10 years old. The experimental materials for the present investigation consisted of 20 genotypes of *Jatropha curcas* developed and maintained at M.R.D.C, Pantnagar. The list of materials has been depicted in **Table 3.1**.

Table 3.1: List of *Jatropha* genotypes used in present investigation

S. No	Genotypes	S. No	Genotypes
1	IGAU, Raipur	11	Indore (SRFI, Jabalpur)
2	IGAU, Bilaspur	12	TFRI-1
3	IGAU, Surguja	13	TFRI-2
4	TNMC-2	14	Pant J. sel-1
5	TNMC-3	15	Pant J.sel-2
6	TNMC-4	16	RJ-117
7	TNMC-5	17	PKVJ-MKV-1
8	TNMC-7	18	PKVJ-DHW-1
9	TNMC-22	19	PJ-03004 (LC-I)
10	Sagar (SFRI, Jabalpur)	20	PJ-03031 (LC-II)

3.2 Experimental design and layout

The study was conducted on 20 different genotypes which were planted during July, 2005 in Randomized Block Design (RBD) with three replications at Medicinal Plant and Development Centre (MRDC) of G.B. Pant university of Agriculture and Technology, Pantnagar. In each replication individual jatropha genotype was represented by twenty plants; plant to plant and row to row spacing was kept (3 × 3) m. The standard agronomic practices were carried out during crop growth period and harvesting of ripe fruits was done December to January month of the year, 2015.

3.3 Morphological parameters

The observations were taken on five selected plants from each row of the each plot. These plants were selected randomly and data were recorded on fourteen quantitative characters which are given below:

Characters	Characters
1. Plant height (m)	8. Number of fruit clusters per plant
2. Collar diameter (cm)	9. Leaf area (cm ²)
3. Number of primary branches	10. Leaf index(l:b ratio)
4. Number of secondary branches	11. Fresh weight of 100 fruits (Kg)
5. Days to flowering(after 31 st July)	12. Dry weight of 100 fruits (Kg)
6. Post floral period (days)	13. 100 seed weight (g)
7. Number of fruits per cluster	14. Seed yield/plant (kg)

3.3.1 Plant Height (m)

The plant height was measured in meter from ground level to tip of main branch at the time of fruit maturity with the help of meter scale.

3.3.2 Collar Diameter (cm)

The circumference of collar of the each randomly selected five plant was measured in centimetre by using measuring tape in the collar region of the tree. From measured value, collar diameter was estimated by using formula:

$$2\pi r.$$

Where,

$$2r = \text{collar diameter}, \pi = 3.14$$

3.3.3 Number of Primary branches per plant

The total numbers of branches which come from the main stem of randomly selected five plants were counted and the average value was worked out at the time of fruit harvest.

3.3.4 Number of Secondary branches per plant

The total numbers of branches which are coming-out from primary branches of the randomly selected five plants were counted and average value was worked out at the time of harvest.

3.3.5 Days to flowering (after 31st July)

Jatropha is a perennial plant and seeds were planted in the field in July, 2005 hence the number of days required for flower initiation from 31st July was recorded. 31st July was considered as day one and its succeeding days were calculated accordingly.

3.3.6 Post floral period (days)

It is the duration from initiation of flowering to fruit maturation (in days). It shows the time of physiological maturity.

3.3.7 Number of fruits per cluster

The total numbers of fruits per cluster from the randomly selected five plants from each replication were counted at the time of fruit maturity and the average numbers of fruits per clusters were recorded.

3.3.8 Number of fruit clusters per plant

All the fruit bearing clusters from randomly selected five plants from each block were counted at the time of fruit maturity and the average numbers of fruit clusters per plant were recorded.

3.3.9 Leaf area (cm²)

The five fully expanded leaves of each randomly selected plant from each replication were taken. The length and width of each leaf was taken with the help of measuring scale in centimetre. The leaf was calculated by using following formula:

$$\text{Leaf area (cm}^2\text{)} = K \times l \times b$$

Where,

$$K = 0.858748 \text{ (Ahmed, 2011)}$$

l = length of fully matured leaf (cm)

b = breadth of fully matured leaf (cm)

3.3.10 Leaf index (l: b ratio)

The leaf length (cm) and width (cm) ratio is calculated of each leaf used for measuring leaf area from each replication and average ratio is calculated up to two decimal.

3.3.11 Fresh weight for 100 fruits (Kg)

One hundred fresh, mature and ripen fruits were harvested from five randomly selected plants from each replication and their average weight was recorded in kilogram up to two points of decimal.

3.3.12 Dry weight for 100 fruits (Kg)

One hundred fruits were picked up at the time of harvestable maturity from the five randomly selected plants from each block manually; sun dried and then weighed on a balance and averaged to get dry fruit yield per hundred fruits. The fruits were harvested three times due to non-synchronous maturity.

3.3.13 100 Seed weight (g)

One hundred dried, sound and disease free seeds were selected randomly from the bulk harvest of each plot and their weight was recorded in grams (g) up to two points of decimal with the help of an electrical balance. Their average was calculated for statistical analysis.

3.3.14 Seed yield per plant (Kg)

All the mature, ripen fruits which were harvested from the five randomly selected plants; sun dried and seeds were shelled out manually from all the dry fruits and seeds were weighted on electronic balance and averaged to get the seed yield per plant in kilogram (kg).

3.4 Statistical analyses

The data recorded on fourteen quantitative characters as given in the section 3.3, were tabulated and the statistical analysis was done under the following statistical procedures:

3.4.1 Analysis of variance (ANOVA)

3.4.2 Estimation of variability parameters

3.4.3 Estimation of genetic divergence

3.4.1 Analysis of Variance

The mean values of observations were recorded on five randomly selected plants from each replication for fourteen quantitative characters on twenty genotypes were subjected to statistical calculation for analysis of variance. The steps involved in the analysis of variance as per suggested by **Panse and Sukhatme (1967)**.

For the analysis of variance under randomized block design, the following linear model was used in the analysis:

$$Y_{ij} = \mu + g_i + r_j + e_{ij}$$

Where,

Y_{ij} = Phenotypic observation of i^{th} entry grown in j^{th} replication,

μ = general mean,

g_i = effect of i^{th} entry,

r_j = effect of j^{th} replication, and

e_{ij} = random error associated with i^{th} genotype in the j^{th} replication.

Total variance is partitioned in to variance due to block (replication), treatment and error and their expectations are given in the **table 3.4.1**.

Table 3.4.1 Analysis of variance

Source of variation	Degree of freedom	Sum of square	Mean square	Expected mean square (EMS)	F-value
Replication	(r-1)	SS _r	MS _r = (SS _r /r-1)	$\sigma_e^2 + t\sigma_r^2$	MS _r /MS _e
Treatment	(t-1)	SS _t	MS _t = (SS _t /t-1)	$\sigma_e^2 + r\sigma_g^2$	MS _t /MS _e
Error	(r-1) (t-1)	SS _e	MS _e = [SS _e /(r-1)(t-1)]	σ_e^2	
Total	(rt-1)				

Where,

r = number of replications

t = number of treatments (genotypes)

SS_r = Sum of square due to replication

SS_t = Sum of square due to treatment

SS_e = Sum of square due to error

MS_r = Mean square for replication

MS_t = Mean square for treatment

MS_e = Mean square for error

Genotypic variance (σ_g^2) = [(MS_t - MS_e)/r]

Phenotypic Variance (σ_p^2) = ($\sigma_g^2 + \sigma_e^2$)

Error variance (σ_e^2) = MS_e

The significance of differences among treatment (genotypic) means will be tested by 'F' test at 5% and 1% level of probability. Wherever the 'F' value found to be significant, critical difference (C.D.) will be calculated to test the significance of difference between treatment mean as follows:

$$CD = SE (d) \times 't' \text{ value at error degree of freedom}$$

Where,

SE (d) = Standard error of difference

$$SE (d) = \pm (2MSe/r)^{1/2}$$

Where,

MS_e = error mean square

r = number of replications

$$\text{Coefficient of variance (CV)} = \sqrt{\text{Error mean square}} / \bar{X} \times 100$$

3.4.2 Estimation of variability parameters

3.4.2.1 Estimation of Coefficient of variability

Analysis of variance permits estimation of phenotypic, genotypic and environmental coefficients of variability. When coefficient of variability is high, the sample is less consistent or more variable and when it is low the sample is more consistent and less variable. Estimation of different coefficient of variability is presented (**Burton and Devane, 1953**) below:

a) Phenotypic coefficient of variation (PCV)

$$PCV \% = \frac{\sigma_{pi}}{\bar{X}} \times 100$$

Where,

σ_{pi} = Phenotypic standard deviation of character 'i'

$\bar{X}$ = general mean of character 'i'

b) Genotypic coefficient of variation (GCV)

$$GCV \% = \frac{\sigma_{gi}}{\bar{X}} \times 100$$

Where,

σ_{gi} = Genotypic standard deviation of character 'i'

$\bar{X}$ = general mean of character 'i'

c) Environmental coefficient of variation (ECV)

$$ECV \% = \frac{\sigma_{ei}}{\bar{X}} \times 100$$

Where,

σ_{ei} = environmental standard deviations of character 'i'

$\bar{X}$ = general mean of character 'i'

3.4.2.2 Estimation of Heritability

Heritability in broad sense was calculated for each character as described by **Johnson *et al.* (1955)** as follows.

$$h^2_{(b)} = \frac{\sigma_{gi}^2}{\sigma_{Pi}^2}$$

Where,

$h^2_{(b)}$ = Heritability in broad sense

σ_{gi}^2 = Genotypic Variance of character 'i'

σ_{Pi}^2 = Phenotypic variance of character 'i'

The genotypic and phenotypic variances are obtained from the expectation of mean squares of analysis of variance of RBD.

3.4.2.3 Estimation of Genetic Advance

The expected genetic advance (GA) under selection for different characters was estimated as suggested by **Allard (1960)**.

$$G.A. = h^2_{(b)} \times \sigma_{pi} \times K$$

Where,

GA = expected genetic advance

$h^2_{(b)}$ = heritability in broad sense

σ_{Pi} = phenotypic standard deviation of character 'i'

K = constant for which the value is given as 2.06 which is the expected in the case of 5% selection intensity. Selection intensity as given by **Lush (1949)**.

Genetic advance was expressed as per cent of population mean for each character as suggested by **Johnson et al., 1955**.

$$\text{Genetic advance as per cent of mean} = \frac{\text{Genetic Advance} \times 100}{GM}$$

3.4.3 Estimation of genetic divergence

3.4.3.1 Estimation of D^2 Value

The genetic divergence in 20 genotypes of jatropha will be estimated by Mahalanobis D^2 statistics (Generalized distance as suggested by **Rao (1952)**). The calculation of D^2 values involved following steps (**Murty and Arunachalam, 1966**).

- i. A set of uncorrelated linear combination (Y_i 's) will be obtained by pivotal condensation of the common dispersion matrix (**Rao, 1952**) of a set of correlated variables (X_i 's; the common dispersion matrix will be arranged with the help of error mean of squares and sum of products).
- ii. Using the relationship between Y_i 's and X_i 's the mean values of different characters (X_1 to X_{13}) will be transformed into the mean values of a set of uncorrelated linear combination (Y_1 to Y_{13}).
- iii. The D^2 values between i^{th} and j^{th} lines for k^{th} character will be calculated as under :

$$D^2_{ij} = \sum_{t=1}^k (Y_{it} - Y_{jt})$$

- iv. The 'K' component and D^2 for each combination will be ranked in descending order of magnitude.

- v. The ranks will be added up for each component. D-square values over all combinations and the rank totals will be obtained.

3.4.3.2 Group constellation

Varieties were grouped into a number of clusters. D^2 was being treated as the square of generalized distance, according to the method described by Tocher (**Rao 1952**). The criterion used in clustering by this method is that any two genotypes belonging to the same cluster showed, at least on an average, show a smaller D^2 value than those belonging to different clusters. In other words, if variety V1 and V2 are close together and variety V3 is distant from both of them as shown by this generalized distance, then V1 and V2 form one cluster. The average D^2 value of all possible combination of genotypes/ varieties in one cluster with those in other was computed and its square root was used to represent the “Statistical distance” between two clusters.

3.4.3.3 Estimation of Contribution to Genetic Divergence

The relative contribution of different characters to the total D^2 between each pair of genotypes will give a score of 1 to 14 (there are 14 characters) based on the magnitude of D^2 values to each characters.

$$\% \text{ Contribution of character 'X'} = \frac{N(X) \times 100}{\text{Total genotypic combination}}$$

$N(X)$ = number of genotypic combinations which ranked 1st for character X out of total genotypic combinations.

$$\text{Total number of possible combination} = \frac{n(n-1)}{2}$$



Results and Discussion



The various plant species that are considered for wealth of India, jatropha possesses an esteem position among them for biofuel production as a substitute of major energy resource obtained from mineral petroleum oil. Naturalized stand of *Jatropha curcas* spreads all over the India and due to varied climatic condition across the country jatropha is likely to have a high degree of variability. **Rao *et al.* (2015)** demonstrated that genotype-environment interaction played significant role towards the expression of different characters in jatropha. The variability studies are the prerequisite and paramount importance for developing tree improvement strategies (**Gariro *et al.*, 2011**). Effective selection thus depends on the existence of sufficient genetic variability in the available breeding material and large variability ensures better chances of producing new combination of genotype in population after recombination of genes between contrast but complementary parent in crossing programme.

Germplasm serve as a most valuable reservoir of variability on which selection can be made directly for evolving superior genotypes or it may be used for compensating nick in otherwise desirable type. The need of evolution and use of diverse germplasm has been emphasized by **Hawkes (1981)**.

In the present investigation twenty open pollinated jatropha genotypes were collected from different geographical regions of India (**Table 3.1**) and the extent of variability, heritability, expected genetic advance and genetic divergence were assessed for yield and different yield contributing traits during 2014-15. The experiment was designed in RBD with three replications.

The experimental results obtained from this investigation have been presented under the following headings:

- 4.1 Analysis of variance and mean performance
- 4.2 Genetic parameters for variability
- 4.3 Genetic divergences (D^2 analysis)

4.1 Analysis of variance and mean performance

4.1.1 Analysis of variance

Analysis of variance based on fourteen characters showed that the mean square values among the genotypes for collar diameter, plant height, primary branches per plant, secondary branches per plant, days to flowering (after 31st July), post floral period (days required for flower initiation to harvest), number of fruits per cluster, number of fruit clusters per plant, leaf area, leaf index (l:b ratio), fresh weight of 100 fruits, dry weight of 100 fruits, 100 seed weight and seed yield per plant were highly significant (**Table 4.1**). This indicated that significant amount of variability existed for fourteen characters among genotypes.

Table 4.1: Analysis of variance for seed yield and yield characters in *Jatropha curcas*.

Traits	Source	Mean sum of square		
		Replication	Genotypes	Error
	d.f.	2	19	38
Plant height (m)		0.032	0.198**	0.005
Collar diameter (cm)		0.963	17.765**	0.944
Primary branches/plant		0.213	4.489**	0.219
Secondary branches/ plant		0.079	24.256**	0.713
Days to flowering (days)		3.738	91.346**	1.409
Post floral period (days)		3.741	91.340**	1.410
Fruits/cluster		0.052	12.322**	0.230
Fruit clusters/plant		0.060	667.258**	0.425
Leaf area (cm ²)		30.590	440.89**	17.922
Leaf index		0.002	0.053**	0.002
Fresh weight of 100 fruits (kg)		0.0001	0.056**	0.001
Dry weight of 100 fruits (kg)		0.0001	0.002**	0.00003
100 seed weight (g)		0.894	43.235**	0.640
Seed yield/plant (kg)		0.0001	0.498**	0.0004

**Significant at 5 per cent level

Other researchers also observed significant variability for yield and related traits (**Singh *et al.*, 2013**), collar diameter, number of branches, fruit yield, seed yield per plant and 100 seed weight (**Tripathi *et al.*, 2013**), number of primary branches per plant, secondary branches per plant, seed yield per plant and 100 seed weight (**Kumar *et al.*, 2015**). **Das *et al.* (2010)** however reported non significance variation for primary branches per plant and fruits per plant which are not in conformity with results of present study. **Saadaoui *et al.* (2015)** also found a wide range of variability for economically relevant traits which are in confirmation with the present study.

4.1.2 Mean performance

Genotypic differences of *Jatropha* are estimated by its range of distribution and mean performance of individual trait. The mean performances of fourteen characters are given in **Table 4.2**.

1. Plant height (m)

A perusal of mean data revealed that the range of plant height was observed to vary between 3.95 to 5.11m with a general mean of 4.68m and the coefficient of variation was 1.452 per cent. The maximum plant height was registered in TNMC-7 (5.11m) followed by Indore (SFRI, Jabalpur), TFRI-2 (4.93m) while minimum plant height was recorded in IGAU Raipur (3.95 m).

2. Collar diameter (cm)

Collar diameter ranged from 30.59 to 40.06cm with general mean 34.484 and the coefficient of variation was 2.819. The maximum collar diameter was attained for PKVJ-MKV-1 (40.06cm) followed by RJ-117 (37.84cm) and PJ-03031 (37.63cm) while minimum collar diameter was observed for IGAU Raipur (30.59cm).

3. Number of primary branches per plant

Primary branches per plant ranged from 6.13 to 11.11 with general mean 8.329. The coefficient of variation for the character was 5.617. The maximum number of primary branches per plant was recorded for IGAU Raipur (11.11) followed by RJ-117 (10.64) and IGAU Bilaspur (9.59), while Sagar SFRI-Jabalpur (6.13) showed the minimum number of primary branches per plant.

Table 4.2: Mean performance of different *Jatropha curcas* genotypes for seed yield and other characters.

Sl. No.	Treatments	Plant height (m)	Collar diameter (cm)	Primary branches/plant	Secondary branches/plant	Days to flowering (after 31 st July)	Post floral period (days)	Fruits/cluster	Fruit clusters/plant	Leaf area (cm ²)	L/B ratio	Fresh weight (Kg) of 100 fruits	Dry weight (Kg) of 100 fruits	100 seed weight (g)	Seed yield/plant (kg)
1	IGAU Raipur	3.95	30.59	11.11	23.87	41.75	90.25	8.54	65.4	136.54	1.02	1.02	0.24	60.42	0.80
2	IGAU Bilaspur	4.34	32.26	9.59	20.06	49.34	82.66	9.28	35.09	154.7	1.02	1.06	0.24	53.22	0.34
3	IGAU Surguja	4.52	32.64	9.01	23.37	50.79	81.21	12.72	62.5	145.79	1.05	1.22	0.25	63.64	1.18
4	TNMC-2	4.34	33.45	9.14	18.22	29.55	102.45	16.52	66.52	157.65	1.03	1.14	0.19	59.42	1.58
5	TNMC-3	4.55	34.97	9.14	20.76	54.46	77.54	18.98	65.41	152.73	1.09	1.13	0.24	56.03	1.76
6	TNMC-4	4.7	34.3	9.08	18.96	52.32	79.68	13.01	26.82	134.77	1.18	0.86	0.22	53.89	0.54
7	TNMC-5	4.68	34.08	7.6	17.05	50.28	81.72	13.36	25.48	148.48	1.06	0.97	0.26	48.87	0.33
8	TNMC-7	5.11	36.17	7.67	17.62	49.05	82.95	16.33	24.25	128.5	1.08	1.1	0.28	48.17	0.25
9	TNMC-22	4.76	37.45	8.54	17.67	49.29	82.71	16.05	21.99	130.93	1.12	1.25	0.27	56.04	0.46
10	Sagar (SFRI,Jabalpur)	4.92	31.73	6.13	14.46	50.49	81.51	13.68	26.08	148.06	1.07	1.04	0.28	58.65	0.35
11	Indore (SFRI,Jabalpur)	4.93	31.95	7.94	17.33	44.97	87.03	14.61	27.62	130.03	1.11	1.29	0.27	52.76	0.40
12	TFRI-1	4.79	34.03	7.78	16.59	51.95	80.05	15.16	41.33	156.96	1.17	0.86	0.26	55.23	0.82
13	TFRI-2	4.93	31.89	7.79	15.44	49.76	82.24	12.57	36.2	123.65	1.09	1.11	0.28	53.89	0.63
14	Pant J. sel-1	4.66	35.29	7.97	15.71	50.49	81.51	13.24	45.32	129.11	1.05	0.76	0.28	56.94	0.71
15	Pant J.sel-2	4.68	34.72	7.48	15.44	53.13	78.87	13.33	54.68	127.56	1.63	1.04	0.28	52.96	1.08
16	RJ-117	4.79	37.84	10.64	22.26	49.58	82.42	12.39	40.3	122.92	1.07	0.9	0.26	56.17	0.60
17	PKVJ-MKV-1	4.66	40.06	7.16	19.72	54.00	78.00	11.89	36.2	123.43	1.10	0.96	0.29	54.67	0.44
18	PKVJ-DHW-1	4.72	35.26	7.04	14.23	51.43	80.57	13.43	45.67	143.37	0.94	0.97	0.28	51.22	0.69
19	PJ-03004 (LC-I)	4.66	33.36	8.4	15.18	53.37	78.63	12.17	51.55	126.28	1.13	0.96	0.28	51.99	0.66
20	PJ-03031 (LC-II)	4.88	37.63	7.34	17.89	51.72	80.28	13.07	48.12	129.82	1.07	0.95	0.27	52.22	0.72
	Grand mean	4.68	34.48	8.33	18.09	49.39	82.61	13.52	42.33	137.56	1.1	1.03	0.26	54.82	0.72
	SEM±	0.39	0.56	0.27	0.49	0.69	0.69	0.29	0.38	2.49	0.26	0.21	0.33	0.46	0.12
	CD 5%	0.11	1.61	0.77	1.4	1.96	1.96	0.82	1.08	7.11	0.74	0.6	0.94	1.32	0.35
	CV (%)	1.45	2.82	5.62	4.67	2.4	1.44	3.69	1.54	3.13	4.09	3.52	2.2	1.46	2.92
	Range	3.95-5.11	30.59-40.06	6.13-11.11	14.23-23.87	29.55-54.46	77.54-102.45	8.54-18.98	21.99-66.52	122.92-157.65	0.94-1.63	0.76-1.25	0.19-0.29	48.17-63.64	0.25-1.76

4. Number of secondary branches per plant

Among genotypes secondary branches per plant ranged from 14.23 to 23.87 with general mean 18.091. The coefficient of variation was recorded 4.665. IGAU Raipur (23.87) had the maximum number of secondary branches per plant followed by IGAU Surguja (23.37) and RJ-117 (22.26). The minimum number of secondary branches per plant was recorded in PKVJ-DHW-1 (14.23).

5. Days to flowering (after 31st July)

Days to flowering (after 31st July) were ranged between 29.55 to 54.46 days. The grand mean and coefficient of variation was 49.386 and 2.40 respectively. The minimum and maximum number of days required for flowering was recorded in TNMC-2 (29.55 days) and TNMC-3 (54.46 days) respectively.

6. Post floral period (days)

Post floral period among *Jatropha* genotypes ranged from 77.54 to 102.45 days with general mean 82.613 days. The coefficient of variation was recorded 1.437. The minimum number of days register for post floral period was noticed in TNMC-2 (77.54 days), while the maximum number of days was observed in IGAU Surguja (102.45 days).

7. Number of fruits per cluster

Number of fruits per cluster ranged from 8.54 to 18.98. Average number of fruits per cluster and coefficient of variation was registered 13.51 and 3.689 respectively. The maximum number of fruits per cluster was recorded for TNMC-3 (18.98) followed by TNMC-2 (16.52) and TNMC-7 (16.33). The minimum number of fruits per cluster was observed for IGAU Raipur (8.54).

8. Number of fruit clusters per plant

The range, grand mean and coefficient of variation for number of fruit clusters per plant was recorded 21.99 to 66.52, 42.33 and 1.539 respectively. The maximum number of fruit clusters per plant was observed for TNMC-2 (66.52) followed by TNMC-3 (65.41) and IGAU Raipur (65.40). The minimum number of fruit clusters per plant was observed for TNMC-22 (21.99).

9. Leaf area (cm²)

Leaf area ranged from 122.92 to 157.65 cm² with general mean 137.56 and coefficient of variation was 3.131. The maximum leaf area was recorded for TNMC-2 (157.65 cm²) followed by TFRI-1 (156.96 cm²) and IGAU Bilaspur (154.7 cm²). The minimum leaf area was recorded for RJ-117 (122.92 cm²).

10. Leaf index (l: b ratio)

Leaf index ranged between 0.94 to 1.63 with general mean 1.10 and coefficient of variation was 4.08. The maximum leaf index was observed for Pant J. sel-2 (1.63) followed by TNMC-4 (1.18) and TFRI-1 (1.17). The minimum leaf index was observed for PKVJ-DHW-1 (0.94).

11. Fresh weight of 100 fruits (Kg)

Jatropha population exhibited a range of 0.756 to 1.29 Kg for fresh weight of hundred fruits, while its general mean and coefficient of variation was registered 1.028 Kg and 3.520 respectively. The maximum fresh weight of hundred fruits was recorded for Indore SFRI Jabalpur (1.290 Kg) followed by TNMC-22 (1.25 Kg) and IGAU Surguja (1.22 Kg). The minimum fresh weight of hundred fruits was observed for Pant J. sel-1 (0.756 Kg).

12. Dry weight of 100 fruits (Kg)

Dry weight of hundred fruits ranged from 0.191 (TNMC-2) to 0.293 Kg (PKVJ-MKV-1) with general mean 0.2595 and coefficient of variation was 2.201. The maximum dry weight of hundred fruits was observed for PKVJ-MKV-1 (0.293 Kg) followed by TNMC-7, Sagar SFRI Jabalpur, TFRI-2, Pant J. sel-1, Pant J. sel-2, PKVJ-DHW-1 and PJ-03031 (0.280 Kg). The minimum dry weight of hundred fruits was recorded for TNMC-2 (0.191 Kg).

13. 100 seed weight (g)

The hundred seed weight ranged from 48.17 to 63.64 g with general mean 54.820 and coefficient of variation was 1.456. The maximum hundred seed weight was recorded for IGAU Surguja (63.64 g) followed by IGAU Raipur (60.42 g) and Sagar SFRI Jabalpur (58.65 g). The minimum hundred seed weight was seen in TNMC-7 (48.17 g).

14. Seed yield per plant (Kg)

Seed yield per plant among jatropha genotypes were found from 0.25 to 1.76 Kg with grand mean 0.717 and coefficient of variation was 2.915. The maximum seed yield per plant was recorded for TNMC-3 (1.76 Kg) followed by TNMC-2 (1.58 Kg) and IGAU Surguja (1.18 Kg). The minimum seed yield per plant was observed for TNMC-7 (0.25Kg).

The superior genotypes over checks (PJ 03004 and PJ 03031), on the basis of overall mean performance for different traits can be exploited directly. Mean performance of table value revealed that TNMC-3, TNMC-2 and IGAU Surguja were significantly superior to seed yield per plant over checks. TNMC-3 also registered higher number of fruit per cluster. TNMC-2 was found to be significantly superior to best check (s) for four traits *viz.*, leaf area, post floral period, number of fruit clusters per plant and days to flowering. IGAU Surguja was found superior for 100 seed weight and secondary branches per plant.

4.2 Genetic parameter for variability

4.2.1 Genetic variance and phenotypic variance

The result of this investigation showed that number of fruit clusters per plant (222.278) registered the maximum value for genetic variance (**Table 4.3**) followed by leaf area (140.991) and days to flowering (29.979). The minimum value for genetic variance was estimated for dry weight of hundred fruits (0.00065). high phenotypic variance was recorded for number of fruit clusters per plant (222.703) followed by leaf area (158.913) and days to flowering (31.388) while the minimum value for phenotypic variance was observed in dry weight of hundred fruits (0.00068). The presence of high genetic and phenotypic variance in population indicated selection would be effective in improving the genetic constitution of cultivar.

In contrast to our study high phenotypic variance and genotypic variance were observed in plant height, seed yield per plant and 100 seed weight by **Shabanimofrad et al. (2013)** and 100 seed weight by **Kaushik et al. (2015)**.

Table 4.3: Estimates of genetic parameters for yield and different yield contributing characters of *Jatropha curcas*.

Characters/ genetic parameter	Plant height (m)	Collar diameter (cm)	Primary branches/ plant	Secondary branches/ plant	Days to flowering (after 31st July)	Post flowering period (days)	Fruits/ cluster	Fruit clusters/ plant	Leaf area (cm ²)	Leaf index	Fresh weight (Kg) of 100 fruits	Dry weight (Kg) of 100 fruits	100 seed weight (g)	Seed yield/ plant (kg)
PCV (%)	5.609	7.422	15.385	16.172	11.344	6.782	15.525	34.994	9.164	12.523	11.73	8.965	7.007	56.79
GCV (%)	5.418	6.867	14.323	15.485	11.087	6.628	15.099	34.96	8.632	11.83	11.678	8.912	6.831	56.571
ECV (%)	0.191	0.555	1.062	0.687	0.257	1.43	0.426	0.034	0.532	0.689	0.049	0.053	0.176	0.2185
h^2_b	93.291	85.583	86.669	91.674	95.51	95.51	94.591	99.801	88.72	89.288	99.17	98.824	95.023	99.736
G A	0.505	4.513	2.288	5.525	11.023	11.02	4.022	30.386	23.04	0.254	250.1	47.979	7.516	0.838
GA as % of the mean	10.78	13.086	27.468	30.541	22.32	13.343	30.252	71.945	16.75	23.034	23.96	18.251	13.71	116.67
V_P	0.069	6.551	1.642	8.561	31.388	22.997	5.927	222.703	158.9	0.019	0.019	0.00068	14.838	0.166
V_g	0.0643	5.607	1.423	7.848	29.979	29.978	5.697	222.278	140.9	0.017	0.018	0.00065	14.198	0.166
v_e	0.005	0.944	0.219	0.13	1.409	1.411	0.23	0.425	17.92	0.002	0.001	0.00003	0.64	0.0004

4.2.2 Phenotypic coefficient of variation (PCV %) genotypic coefficient of variation (GCV %) and environmental coefficient of variation (ECV %)

The Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for the various traits were evaluated. The estimates of PCV, GCV and ECV are presented in **Table 4.3**. It is apparent from this table that phenotypic coefficient variation was generally higher than genotypic coefficient of variation for all the characters studied. Seed yield per plant showed the highest phenotypic coefficient of variation (56.79 %) followed by number of fruit clusters per plant (35.258%), number of secondary branches per plant (16.172%), number of fruits per cluster (15.525%) and number of primary branches per plant (15.358%). The lowest phenotypic coefficient of variation was observed for plant height (5.609%). Seed yield per plant exhibited the highest genotypic coefficient of variation (56.571%) followed by number of fruit clusters per plant (35.224%), number of secondary branches per plant (15.485%), number of fruits per cluster (15.099%), number of primary branches per plant (14.323%). The lowest genotypic coefficient of variation (5.418%) was observed for plant height. The range of environmental coefficient of variation was registered 0.034% (number of fruit clusters per plant) to 1.43% (post floral periods). These results indicated that variability was primarily due to genotypic differences. Therefore, selection based on these characters is expected to be effective.

Similar studies with respect to PCV and GCV were carried out by various workers. Our result was also good agreement with **Shabanimofrad *et al.*, (2013)** who observed high PCV and GCV values for seed yield per plant, number of primary branches, number of fruits per cluster, plant height and hundred seed weight except plant height, hundred seed weight. **Kaushik *et al.* (2015)** observed high PCV and GCV for 100 seed weight which is not in confirmation with the present study. The result of **Das *et al.* (2010)** bear close affinity to our findings for seed yield per plant, number of fruits per plant and secondary branches per plant (with high PCV and GCV), collar diameter, plant height and 100 seed weight (with low PCV and GCV).

4.2.3 Heritability and Genetic advance

The heritability refers to an index of transmissibility of genetic influence upon expression of a trait of an individual from one generation to its next generation. It measures the genetic relationship between the parents and their offspring. Effective

selection depends on the existence of the genetic variability in heritability of a trait. Experimental analysis found that very high heritability for number of fruit clusters per plant (99.809%) followed by seed yield per plant (99.736%), 100 seed weight (95.688%), days to flowering (95.51%), post flowering period (95.51%), dry weight of 100 fruits (95.246%), number of fruits per cluster (94.591%), fresh weight of 100 fruits (93.326%), plant height (93.291%), number of secondary branches per plant (91.674%), leaf index (89.288%), leaf area (88.722%), and number of primary branches per plant (86.669%). The lowest value of heritability was found for collar diameter (85.583%). Most of the traits included in this investigation were considered highly heritable as they have shown to be associated with high value of broad sense heritability.

Heritability for different traits in jatropha was estimated by different workers. The results on heritability of different traits described by **Shabanimofrad *et al.* (2013)** accorded to our findings for primary branches and 100-seed weight except collar diameter. **Das *et al.*, (2010)** reported high heritability for plant height and 100 seed weight but moderate heritability was found for collar diameter, secondary number of branches per plant and seed yield per plant.

Heritability and genetic advance are the important genetic parameters. The knowledge of heritability coupled with expected genetic advance will help in deciding the scope for improvement of a trait through selection (**Johnson *et al.*, 1955**). The range of genetic advance was from 0.254 to 30.683. The maximum value for genetic advance was calculated for fruit clusters per plant (30.683) followed by leaf area (23.04) and days to flowering, post flowering period (11.02). Expected genetic advance indicates the expected genetic progress for a particular trait under a selection cycle and measures the extent of its stability under selection pressure.

The range of genetic advance as per cent of mean recorded high for seed yield per plant (116.678%), number of fruit clusters per plant (72.92%), number of secondary branches per plant (30.541%), number of fruits per cluster (30.252%), number of primary branches per plant (27.468%), fresh weight of 100 fruits (26.192%), leaf index (23.034%), and flowering duration after 31st July (22.320%) while moderate estimates were found for dry weight of 100 fruits (19.809%), leaf area (16.749%), 100 seed weight (13.851%), collar diameter (13.086%) and plant height

(10.78%). Heritability, genetic advance and genetic advance as per cent of mean are important genetic parameters for the selection of desirable traits.

Kaushik *et al.* (2007) found high heritability (broad sense) and genetic gain fruit seed ratio (99.00%, 87.78%), 100 seed weight (100.0%, 66.99%), 100 fruit weight (98.00%, 57.38%) respectively indicate additive gene action in *Jatropha curcas*. High heritability revealed that the expression of a trait largely depend on genetic components while the influence of environment was found less. Estimates of high heritability with high genetic advance for seed yield per plant, number of fruits per plant and secondary branches per plant were observed by **Das *et al.* (2010)**. Similarly, high estimates of heritability with high genetic advance for plant height and number of fruits per plant were reported by **Singh *et al.* (2013)** and **Tripathi *et al.* (2013)** indicating the additive genetic control in the inheritance of these traits suggesting that early generation phenotypic selection would be effective for these traits.

4.3 Genetic Divergence Analysis

The analysis of variance showed highly significant differences among the twenty genotypes for the fourteen characters (**Table 4.1**). This indicated the existence of significant variability among the genotypes for all the characters studied. The divergence was estimated by Mahalanobis D^2 statistic as described by **Rao (1952)**. Based on D^2 values, the grouping of genotypes into different clusters was done according to Tocher's method (**Rao, 1952**).

4.3.1 Grouping of genotypes into clusters

In the present investigation all the twenty genotypes for fourteen characters grouped into three clusters. The clustering pattern of genotypes is given in **Table 4.4**. The cluster I had three genotypes viz., IGAU-Raipur, IGAU-Surguja and TNMC-3, while the cluster II had sixteen genotypes viz., IGAU- Bilaspur, TNMC-4, TNMC-5, TNMC-7, TNMC-22, Sagar (SFRI, Jabalpur), Indore (SFRI, Jabalpur), TFRI-1, TFRI-2, Pant J. sel-1, Pant J. sel-2, RJ-117, PKVJ-MKV-1, PKVJ-DHW-1, PJ-03004 (LC-I), PJ-03031 (LC-II). Cluster III however represented by single genotype (TNMC-2).

Table 4.4: Clustering patterns of twenty genotypes on the basis of D² values in *Jatropha curcas*

Cluster number	Genotypes included	Number of genotypes
I	IGAU Raipur, IGAU Surguja, TNMC-3	3
II	IGAU Bilaspur, TNMC-4, TNMC-5, TNMC-7, TNMC-22, Sagar (SFRI, Jabalpur), Indor (SRFI, Jabalpur), TFRI-1, TFRI-2, Pant J. sel-1, Pant J. sel-2, RJ-117, PKVJ-MKV-1, PKVJ-DHW-1, PJ-03004 (LC-I), PJ-03031 (LC-II)	16
III	TNMC-2	1

It was presumed those identical genotypes or the genotypes which were genetically close to each other fall in the same cluster and exhibited similar morphological characters. In the present investigation it was revealed that genotypes were collected from different regions in India were grouped in to same cluster. All the three genotypes in cluster I originated from different geographical region. Similarly sixteen genotypes including two checks (*viz.*, PJ-03004 and PJ-03031) of diverse origin were grouped in to cluster II. It was therefore apparent that genotypes from same geographical locations fell into different clusters as well as genotypes from different geographical locations fell into same cluster indicating that clustering of populations did not follow their geographic distribution. Similar observations have been reported by **Gohil and Panda (2008)** and **Singh *et al.* (2013)**. Different clustering pattern were also reported recently on *Jatropha* by some workers (**Gohil and Panda, 2008; Singh *et al.*, 2013** and **Kaushik *et al.*, 2015**).

The pattern of group constellation proved that geographical diversity need not necessarily be related to the genetic diversity since lines of *jatropha* originating from same geographical region tend to fall into different cluster and the genotypes included in the same cluster had different geographical region.

4.3.2 Average intra and inter cluster distances

Intra and inter cluster average D^2 -values and genetic distances (D) are given in **Tables 4.5**. The intra-cluster average D^2 values ranged from 0.00 to 15.651. It was found maximum in cluster II (15.651) with sixteen genotypes followed by cluster I (10.937) with three genotypes. The minimum intra-cluster distance was found for Cluster III (0.000) which was represented by only one genotype. The inter-cluster average D^2 - value was found maximum between cluster II and III (48.504). Average D^2 -value between clusters I and II and between cluster I and III registered 30.963 and 30.854 respectively.

Table 4.5: Average inter and intra-cluster (diagonal) D^2 values in *Jatropha curcas*

Clusters	I	II	III
I	10.937	30.963	30.845
II		15.651	48.504
III			0.000

The relative genetic distance (D), as calculated by taking square root of D^2 -values, between different clusters are presented in **Table 4.6**. The highest genetic distance was found between cluster II and III (6.964) indicating that genotypes belong to these two cluster were genetically more diverse in comparison to that observed between cluster I and III (5.554) and between cluster I and II (5.564). The genotypes belong to clusters I maintained equal distance from both cluster II and cluster III.

Table 4.6: Average inter and intra-cluster (diagonal) D values in *Jatropha curcas*

Clusters	I	II	III
I	3.307	5.564	5.54
II		3.956	6.964
III			0.000

These results therefore suggested that the genotypes from divergent clusters can be inter-crossed to obtain high heterotic response and also to recover desirable transgressive- segregants as discussed earlier. **Gohil *et al.* (2008)** and **Singh *et al.* (2013)** also arrived to the similar conclusion that use of divergent parent exhibited heterotic response through favourable combination of genes from two divergent, contrast but complementary parents in a cross, which help to produce superior plants through transgressive segregation.

4.3.2 Cluster means and contribution of individual character toward divergence

Cluster mean values for fourteen characters are given in **Table 4.7**. This would give us an opportunity to identify genotypes with superior traits for seed yield and other component character, to create further variability for these characters and to use these genotypes in future breeding programmes as donor of these characters (**Table 4.9**). A perusal of data showed considerable difference exists among cluster means for all characters. Cluster I with three genotypes exhibited higher cluster mean values for number of primary branches per plant (9.756), number of secondary branches per plant (22.667), hundred seed weight (60.03g). Cluster II showed highest cluster mean values for plant height (4.765m), collar diameter (34.876 cm), days to flowering (50.698 days), leaf index (1.118), and dry weight of hundred fruits (0.267 Kg). The lowest cluster mean values for days to flowering (29.55 days) and post flowering period (102.45 days) also recorded in cluster II while the highest cluster mean values for number of fruits per cluster (16.52), number of fruit clusters per plant (66.57), leaf area (157.65cm²), 100 seed weight (59.54g) and seed yield (1.58 Kg) were obtain in cluster III.

The relative contribution of these characters towards the expression of genetic divergence (**Table 4.8**) revealed that seed yield per plant exerted maximum influence towards genetic divergence (25.637%) followed by number of fruits per cluster (15.927%), post flowering period (7.963%), number of secondary branches (7.103%), number of primary branches (6.638%), leaf index (6.012%). These characters were considered to be the most important for creating genetic diversity in *Jatropha* population. Experimental results revealed that plant height (2.475%), hundred seed weight (3.019%), dry weight of 100 fruits (3.130%), collar diameter (3.190%), no. of fruit clusters per plant (3.983%) and fresh weight of hundred fruits (4.397%) contributed minimum towards the expression of genetic divergence in *jatropha* population.

Table 4.7 Cluster mean values for fourteen characters in *Jatropha curcas*

Character	Cluster		
	I	II	III
Plant height (m)	4.341	4.765	4.343
Collar dia. (cm)	32.732	34.876	33.445
No. Of primary branches	9.756	8.012	9.144
No of secondary branches	22.667	17.226	18.217
Days to flowering (days)	49	50.698	29.55
post flowering period	83	81.302	102.45
No. of fruits /cluster	13.415	13.347	16.522
No. of fruit clusters/ plant	64.435	36.669	66.517
Leaf area (cm ²)	145.02	134.91	157.65
Leaf index (l: b ratio)	1.053	1.118	1.027
Fresh weight of 100fruits (Kg)	1.125	1.004	1.136
Dry weight of 100 fruits (Kg)	0.242	0.267	0.191
100 seed weight (g)	60.03	53.556	59.417
Seed yield / plant (kg)	1.25	0.564	1.58

Table 4.8: Contribution of fourteen characters towards divergence in *Jatropha curcas*

Sl. No.	Characters	Contribution (percentage)
1	Plant height (m)	2.475
2	Collar diameter (cm)	3.190
3	No. Of primary branches	6.638
4	No of secondary branches	7.103
5	Days to flowering (days)	5.050
6	Post flowering period	7.963
7	No. of fruits per cluster	15.927
8	No. of fruit clusters per plant	3.983
9	Leaf area (cm ²)	5.474
10	Leaf index (l:b ratio)	6.012
11	Fresh weight of 100fruits (Kg)	4.397
12	Dry weight of 100 fruits (Kg)	3.130
13	100 seed weight (g)	3.019
14	Seed yield per plant (kg)	25.637

Table: 4.9 Donors for different traits in *Jatropha curcas*

Sl. No.	Character	Donors
1	Plant height (m)	Indore (SFRI, Jabalpur), TFRI-I, PJ-03031, RJ-117 and TFRI-II
2	Collar diameter (cm)	PKVJ-MKV-1, RJ-117, PJ-030031, Pant J. sel-1, PKVJ-DHW-1
3	Primary branches/plant	IGAU Raipur
4	Secondary branches/ plant	IGAU Raipur and IGAU Surguja
5	Days to flowering (after 31st July)	IGAU Surguja, TNMC-3, TNMC-4, TFRI-1, Pant J. sel-2, PKVJ-MKV-1, PKVJ-DHW-1, PJ-03004 and PJ-03031
6	Post flowering period (days)	TNMC-2
7	Fruits/cluster	TNMC-2
8	Fruit clusters/plant	TNMC-2
9	Leaf area (cm ²)	TNMC-2
10	L:B ratio	TNMC-4, Pant J. sel-2 and PJ-03004
11	Fresh weight (Kg) of 100 fruits	TNMC-2
12	Dry weight (Kg) of 100 fruits	PJ-03031, PJ-03004, PKVJ-DHW-1, PKVJ-MKV-1, TFRI-2, Pant J. sel-1 and Pant J. sel-2
13	100 seed weight (g)	TNMC-2
14	Seed yield/ plant (kg)	TNMC-2

The study on genetic divergence by **Gohil *et al.* (2008)** did not accord to our observations except seed yield. This suggested that relative variability of cluster mean among traits were partly associated with genetic constitution of individual jatropha plant and partly by the influence of environment at growing site. **Yang *et al.* (2007)**, **Malaipan *et al.* (2008)** and **Luo *et al.* (2011)** described that morphological variability in jatropha populations possibly originated through differences in ecological adaptations fruit sets, variability in floral biology, pollination mechanism, suitable availability of pollinating agents and its behaviour

In summing up the results of this investigation and to make a comparative assessment of mean performance of individual jatropha genotypes for each trait (**Table 4.2**) and cluster mean values (**Table 4.7**) three lines *viz.*, IGAU Raipur, TNMC 3 (both from cluster I) and TNMC2 (cluster III) were found promising and could be utilized as parent in a cross to produce new genotypes with superior combination of traits for augmenting seed yield per plant of jatropha population.

*Summary
and
Conclusion*

Limited availability of petroleum oil coupled with the gradual shrinking of resources and current hike in petroleum oil prices draws the greater awareness among scientists to search for alternative resource of petroleum oil all over the world. It has now apparent that the major resource of bio diesel may be possibly extracted from fatty acid composition store in the seeds of many cultivated and wild plant species. *J. curcas* is one of such precious tree and grown in semi-wild state in different regions of India. The seeds of plant are used for extraction of biodiesel as a substitute of mineral petroleum oil.

In the present investigation genetic variability and genetic divergence analysis was carried out based on morphological characters in *Jatropha curcas* with the following objectives:

1. To estimate relative morphological variability and genetic divergence present in different characters among jatropha genotypes.
2. To determine heritability (h^2) and genetic advance (GA) for various morphological characters.

The twenty genotypes of *J. curcas* were collected from different regions of the country. These genotypes were evaluated at the Medicinal Research and Development Centre of the G. B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand, India for fourteen morphological characters viz. plant height (m), collar diameter (cm), primary branches per plant, secondary branches per plant, days to flowering (after 31st July), post floral period (days), number of fruits per cluster, number of fruit clusters per plant, leaf area (cm^2), leaf index (l:b ratio), fresh weight (Kg) of 100 fruits, dry weight (Kg) of 100 fruits, 100 seed weight (g) and seed yield (Kg) per plant. The seed of jatropha genotypes were planted on July, 2005 in Randomized Block Design with three replications. Each plot had one row with twenty plants. The spacing between plant to plant and row to row was kept 3×3 m. During crop growth period standard agronomic practices were carried out to obtain good plant stand, disease and insect free plants. Fruits were harvested during month of

December-January. Field data of the present investigation were obtained from ten years old plant during 2014-15. The observations were recorded on five randomly selected plants. The mean values of all the characters were subjected to statistical analysis to draw the conclusions.

The ANOVA values were used to estimate genetic variance, phenotypic variance and environment variance of each trait. The genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and environment coefficient of variation (ECV) were computed as given by **Burton and Devane (1953)**. Heritability in broad sense was calculated as a ratio of genotypic variance to phenotypic variance and expressed in percentage as given by **Allard (1960)**. The genetic advance and the genetic gain over per cent of mean were calculated according to formula developed by **Johnson *et al.* (1955)**.

The presence of genetic diversity is the basic requirement for developing elite genotypes through effective selection and crossing programme. Hence the genetic divergence in twenty genotypes of *J. curcas* was estimated by Mahalanobis D^2 statistic (generalized distance as suggested by **Rao (1952)**).

The special features of the present investigation are summarized as follows:

- ❖ In ANOVA mean squares due to genotype were highly significant for all of the characters indicating the presence of significant variability among genotypes for all the characters, which offer sufficient scope for further improvement in seed yield and its component traits.
- ❖ The variability of individual trait was marked by the distribution of its range, which was again influenced by the unit of its measurements. The CV has no unit so it could be used to measure relative dispersion among traits. The maximum and minimum dispersion of CV value was observed in primary number of branches and post floral period respectively.
- ❖ The highest phenotypic variance and genotypic variance was registered for number of fruit clusters per plant followed by leaf area, days to flowering and post floral period, whereas low phenotypic variance was estimated for fresh weight of 100 fruits, leaf index, plant height and seed yield per plant.

- ❖ The maximum value of genotypic coefficient of variation and phenotypic coefficient of variation were registered for seed yield per plant followed by number of fruit clusters per plant, number of secondary branches per plant, number of fruits per cluster and number of primary branches per plant, whereas low genotypic coefficient of variation estimated for collar diameter, plant height, post floral period and 100 seed weight.
- ❖ Environmental coefficient of variation appeared low for all characters suggesting that these characters are less influenced by the environment and stable in expression.
- ❖ High level of broad sense heritability was observed for all characters. This ensures that genetic variance was associated with transmission of characters from one generation to next generation.
- ❖ Higher values of genetic advance was recorded for fresh weight of 100 fruits, dry weight of 100 fruits, number of fruit cluster per plant, leaf area, days to flowering and post floral period. This suggested that genetic improvement for traits could be possible through selection.
- ❖ High estimates of genetic gain over percent of mean were achieved by seed yield per plant followed by number of fruit clusters per plant, number of secondary branches per plant, number of fruits per cluster, number of primary branches per plant, fresh weight of 100 fruits and days to flowering. While, moderate estimates of genetic gain over percent of mean were recorded for dry weight of 100 fruits, leaf area, 100 seed weight, post floral period, collar diameter, plant height indicating that the selection could be effective to gain expected genetic progress for these characters under selection cycle.
- ❖ The study on genetic parameters thus revealed that day to flowering, number of fruit clusters per plant and 100 seed weight were controlled by additive gene effect as it exhibited moderate to high values for genetic variance, GCV, heritability, genetic advance and genetic gain over percent of mean.
- ❖ The twenty genotypes were grouped into three clusters based on D^2 statistic. The maximum number of genotypes sixteen (IGAU Bilaspur, TNMC-4, TNMC-5, TNMC-7, TNMC-22, Sagar (SFRI, Jabalpur), Indore (SFRI,

Jabalpur), TFRI-1, TFRI-2, Pant J. sel-1, Pant J. sel-2, RJ-117, PKVJ- MKV- 1, PKVJ-DHW-1, PJ-03004(LC-I), PJ-03031(LC-II) were grouped in the cluster II followed by cluster I with three genotypes (IGAU Raipur, IGAU Surguja, TNMC-3) and cluster I had only one genotype (TNMC-2).

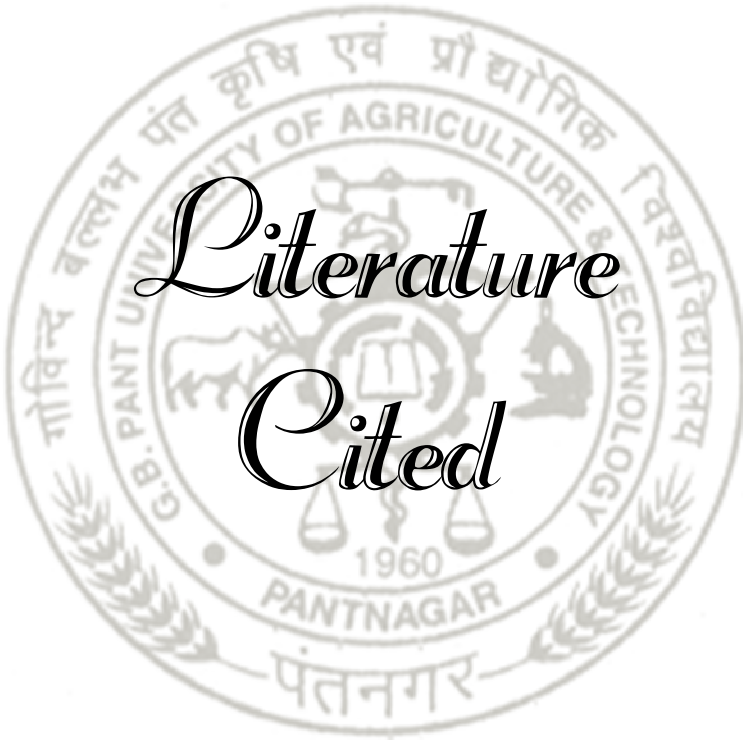
- ❖ On the basis of D^2 estimates, maximum divergence was found between the genotypes of cluster II and III. The inter-cluster distance between I and II appeared almost equal to that of recorded between clusters I and III.
- ❖ The pattern of genetic diversity showed that eco-geographical diversity may not be necessarily related to the genetic diversity. It could be seen from the group constellation that genotypes having same origin and similar morphological characters fall into separate clusters, while genotypes having different origin and morphological character were included in one cluster. The two check varieties, under study, were grouped into same clusters. It means even they are geographical diverse but share same genetic constitution. Thus genetic diversity rather than geographical diversity should be considered on priority for the selection of superior parents. These parents can be used for development of superior hybrid.
- ❖ The genotypes in cluster I had maximum number of primary branches per plant, number of secondary branches per plant, 100 seed weight. The genotypes in the cluster II had maximum plant height, collar diameter, days to flowering, leaf index and dry weight of 100 fruits. The genotypes in the cluster III had maximum post floral period, number of fruits per cluster, number of fruit clusters per plant, leaf area, fresh weight of 100 fruits and seed yield per plant.
- ❖ Seed yield per plant contributed maximum towards genetic divergence followed by number of fruits per cluster, post floral period, number of secondary branches per plant, number of primary branches per plant, leaf index, leaf area, days to flowering and fresh weight of 100 fruits. These characters were thought to be the more important for constituting genetic diversity in the population and could be utilized in the effective breeding programme to achieve desire genetic gain.

- ❖ In this present investigation selection of IGAU Raipur, IGAU Surguja, TNMC-3 (from cluster I) and TNMC-2 (cluster III) as a parent in hybrid programme may contribute more to augment the seed yield of jatropha genotypes.

CONCLUSION

On the basis of present findings it can be concluded that significant genotypic differences on morphological characters exist in jatropha population under study. The analysis of variance showed significant genetic variability and less coefficient of variation in all the characters indicating good precision of the experiment. High values for genetic variance, GCV, heritability, genetic advance and genetic gain over per cent of mean observed in days to flowering, number of fruit clusters per plant and 100 seed weight and suggested that these characters are most suitable for selection. The expression of other morphological traits was presumed to be governed by non-additive gene effects with high level of genotype and environment interactions. There was no correlation between geographical distribution of genotypes and genetic diversity because genotypes were obtained from different locations, gets cluster in same group. This kind of genetic diversity may be due to selection pressure, differential adoption, selection criteria, environment and genetic drift. In plant breeding, genetic diversity plays an important role because hybrids between lines of diverse origin display a greater heterosis than those between closely related parents. Hence, judicious choice of parents from cluster analysis and proper exploitation of gene effect of individual trait seems to improve the seed yield of jatropha genotype.

A comparison between mean value of individuals and cluster mean values revealed that three lines viz., IGAU Raipur, TNMC-3 and TNMC-2 found promising and could be used for hybridization programme for development of superior genotype.



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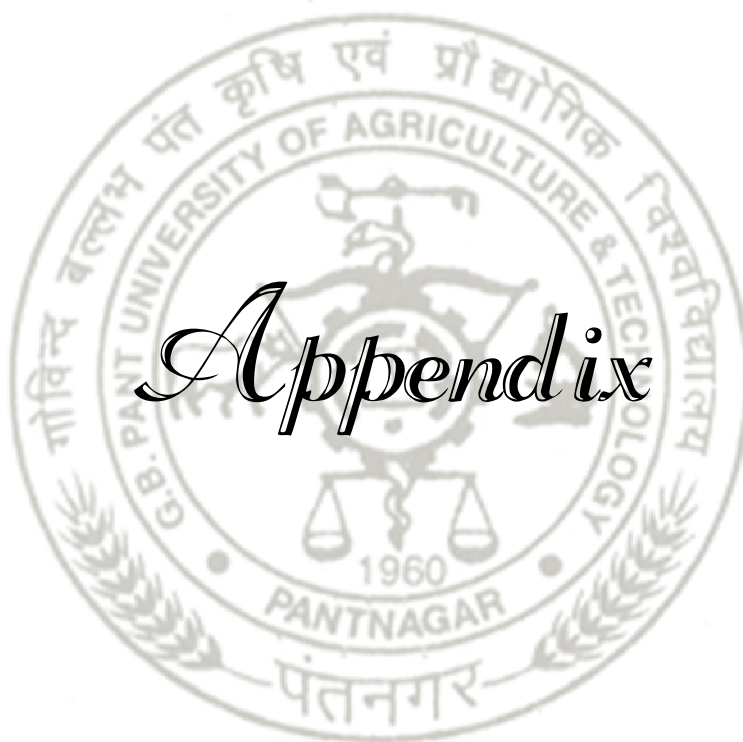
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Appendix



APPENDIX-I

Standard meteorological week's and average weather data from October 2015 to January 2016 at G.B.P.U.A. & T. Pantnagar-263145

Month	Date	Year	Metro Week No. (2012)	Temperature (°C)		Relative Humidity (%)		Rainfall (mm)	No. of Rainy Days	Sun-Shine Hrs.	Wind Velocity (km/hr.)	Evap. (mm)
				Max.	Min.	0712 am	1412 pm					
May-Jun	28-03	2015	22	39.7	22.2	65	31	Tr.	0	08.1	6.3	9.2
Jun	04-10	2015	23	41.4	24.5	62	30	000.0	0	09.9	9.2	11.5
Jun	11-17	2015	24	37.3	25.6	62	37	000.8	0	06.9	7.6	10.1
Jun	18-24	2015	25	34.9	26.5	73	54	166.4	4	06.1	7.4	4.9
Jun-Jul	25-01	2015	26	31.4	23.8	90	76	230.8	3	04.3	7.6	4.2
Jul	02-08	2015	27	32.7	25.7	87	72	111.0	4	04.2	6.9	3.4
Jul	09-15	2015	28	32.0	25.4	88	72	184.6	5	04.6	7.3	4.5
Jul	16-22	2015	29	32.5	26.6	84	72	009.8	2	04.1	5.9	4.2
Jul	23-29	2015	30	33.8	25.9	83	63	006.4	2	09.3	7.3	5.7
Jul-Aug	30-05	2015	31	31.4	25.7	87	74	148.8	4	03.6	5.2	2.8
Aug	06-12	2015	32	30.4	25.4	91	76	089.9	4	03.3	5.0	4.1
Aug	13-19	2015	33	32.6	26.1	90	67	050.6	3	04.2	4.7	3.2
Aug	20-26	2015	34	32.4	24.9	89	69	028.6	3	05.2	5.8	4.0
Aug-Sep	27-02	2015	35	33.3	25.4	92	65	022.2	1	06.8	5.6	4.7
Sep	03-09	2015	36	33.7	23.9	91	60	000.0	0	08.2	4.5	7.1
Sep	10-16	2015	37	34.1	25.0	87	59	Tr	0	08.1	3.0	4.6
Sep	17-23	2015	38	33.6	24.9	84	62	112.0	1	05.8	4.8	4.1
Sep	24-30	2015	39	32.1	21.7	90	61	000.0	0	09.2	3.8	4.2
Oct	01-07	2015	40	32.9	20.2	83	51	000.0	0	09.5	2.1	4.7
Oct	08-14	2015	41	32.5	20.3	83	52	000.0	0	07.5	2.4	4.6
Oct	15-21	2015	42	31.5	19.3	86	51	000.0	0	05.1	3.1	3.5
Oct	22-28	2015	43	31.2	13.9	88	48	000.0	0	08.7	3.0	4.0
Oct-Nov	29-04	2015	44	29.0	13.7	90	43	005.0	1	06.2	2.9	3.0
Nov	05-11	2015	45	28.0	12.1	91	43	002.0	1	06.6	3.0	2.5
Nov	12-18	2015	46	29.0	11.9	91	38	000.0	0	07.8	2.8	2.7
Nov	19-25	2015	47	27.7	11.3	92	41	000.0	0	07.2	1.6	2.3
Nov-Dec	26-02	2015	48	26.7	12.6	91	46	000.0	0	03.7	2.7	2.1
Dec	03-09	2015	49	24.6	10.2	96	49	000.0	0	01.8	2.3	1.6
Dec	10-16	2015	50	21.1	10.3	94	64	000.0	0	02.1	4.3	1.3
Dec	17-23	2015	51	20.5	4.6	96	50	000.0	0	05.3	2.5	1.5
Dec	24-31	2015	52	21.0	5.0	95	46	000.0	0	06.1	3.0	1.5
Jan	01-07	2016	1	23.6	6.9	92	39	000.0	0	06.0	2.7	1.5
Jan	08-14	2016	2	22.3	7.0	94	49	000.0	0	04.3	3.3	1.7
Jan	15-21	2016	3	17.4	6.6	94	64	000.0	0	02.3	4.6	1.4
Jan	22-28	2016	4	17.9	4.1	94	53	000.0	0	03.3	3.2	1.3
Jan-Feb	29-04	2016	5	22.2	6.8	96	48	000.0	0	04.8	5.3	1.9

The author of this manuscript was born on 1 July 1991. He passed High School and Intermediate examination from Swami Dayanand Saraswati Senior Secondary School, Nadbai (Rajasthan) in 2005 and 2007 respectively. He has completed his graduation (B. Sc. Agriculture) from U.A.S, Dharwad in the year 2014. Later, he joined M.Sc. Agriculture (Genetics and Plant Breeding) in the G. B. Pant University of Agriculture and Technology, Pantnagar (U. S. Nagar), Uttarakhand, in the same year 2014.

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ABSTRACT

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Jatrophacurcas is used for production of biodiesel, waste land management, medicinal purposes etc. In this present investigation emphasis has given to study the “Genetic variability and divergence analysis in *J. curcas* L. based on morphological characters” among ten years old twenty genotypes, which were collected from different regions of India and planted on 27-29 July, 2005 in Randomized Block Design with three replications at Medicinal Plant Research and Development Centre, G.B. Pant University of Agriculture and Technology, Pantnagar, India. The standard agronomic practices were carried out during crop growth period to obtain good plant stand and disease and insect-pest free plants. Data were recorded during 2014-15 on five randomly selected plants from each plots of each genotype separately. The observations were recorded on fourteen characters viz., plant height (m), collar diameter (cm), number of primary branches per plant, number of secondary branches per plant, days to flowering (after 31st July), post floral period (days), number of fruits per cluster, number of fruit clusters per plant, leaf area (cm²), leaf index, fresh weight of hundred fruits (kg), dry weight of hundred fruits (kg), 100 seed weight (g) and seed yield per plant (kg).

The ANOVA revealed highly significant differences among genotypes for all characters. The study on genetic parameters showed high genetic variance, genetic coefficient of variation, heritability, genetic advance and genetic gain over percent of mean for days to flowering, fruit clusters per plant and fresh weight of 100 fruits suggested the preponderance of additive genetic control for these traits.

Twenty genotypes on D² analysis were grouped into three clusters. Cluster I comprised of three genotypes with higher cluster mean value for primary and secondary branches per plant. Sixteen genotypes constituted cluster II showing higher mean values for plant height, collar diameter and days to flowering. One genotype represented cluster III and exhibited high mean values for post floral period, fruits per cluster. The maximum inter-cluster distance was found between cluster II and III; and minimum inter-cluster distance was found between cluster I and III, while cluster I was separated from cluster II and III by equal distance. Experimental results revealed that seed yield/plant, fruits/cluster and post floral period had contributed maximum towards genetic diversity and the genetic diversity was not associated with geographical diversity of *Jatropha* genotypes.

Hence, genotypes with potential genetic diversity viz., IGAU Raipur, IGAU Surguja, TNMC-3 (from cluster I) and TNMC-2 (cluster III) can be used as a parent in hybrid cross to improve genetic constitution towards augmenting the productivity of seed yield in *Jatropha* population.

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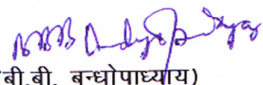

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शोध ग्रंथ शीर्षक	: "जेट्रोफा कर्कस एल की रूपात्मक लक्षणों पर आधारित आनुवांशिक परिवर्तनशीलता और विचलन विश्लेषण"		

जेट्रोफा कर्कस बायोडीजल के उत्पादन, अपशिष्ट भूमि प्रबंधन एवं औषधीय प्रयोजनों आदि के लिए प्रयोग किया जाता है। इस वर्तमान जांच में दस वर्ष आयु वाले जेट्रोफा कर्कस के बीस जीनोटाइप की रूपात्मक लक्षणों पर आधारित आनुवांशिक परिवर्तनशीलता और विचलन विश्लेषण का अध्ययन करने के लिए प्रमुखता दी गई। वे भारत के विभिन्न क्षेत्रों से एकत्र किए गए और 27-29 जुलाई, 2005 को औषधीय पादप अनुसंधान एवं विकास केंद्र, गोविंद वल्लभ पंत कृषि एवं प्रौद्योगिकी विश्वविद्यालय, पंतनगर में तीन अनुकरण के साथ यादृच्छिक ब्लॉक डिजाइन में लगाए गए थे। मानक कृषि पद्धतियों का उपयोग उपयुक्त पादप ठहराव और रोग एवं कीट मुक्त पादप प्राप्त करने के लिए फसल की अवधि के दौरान किया गया। प्रत्येक भूखंड के, हर जीनोटाइप से पाँच क्रमरहित चयनित पौधों पर 2014-15 वर्ष के दौरान आकड़े लिए गए। चौदह लक्षणों के अवलोकन दर्ज किए गए, वे हैं: पौधे की ऊँचाई (मीटर), कॉलर व्यास (सेमी), प्रति पादप प्राथमिक शाखाओं की संख्या, द्वितीय शाखाओं की संख्या प्रति पादप, फूल आने के दिनों की संख्या (31 जुलाई के बाद), फूल अवधि के बाद के दिनों की संख्या (दिन), प्रति समूह फलों की संख्या, प्रति पादप फल समूहों की संख्या, पत्ती क्षेत्र (सेमी²), पत्ती सूचकांक, सौ ताजा फलों का वजन (किलो), सौ सुखे फलों का वजन (किलो), सौ बीजों का वजन (ग्राम) एवं बीज उपज प्रति पादप (किलो)। एनोवा के द्वारा सभी जीनोटाइप के बीच अति अभिप्रायपूर्ण अंतर पाया गया।

आनुवांशिक मापदंडों के अध्ययन से ज्ञात होता है कि फूल आने के दिनों की संख्या, प्रति पादप फल समूहों की संख्या एवं सौ ताजा फलों का वजन के लिए उच्च आनुवांशिक विचरण, आनुवंशिक गुणांक का परिवर्तन, आनुवंशिकता, आनुवंशिक अग्रिम और प्रतिशत से अधिक आनुवांशिक लाभ उच्च पाया गया जो यह दर्शाता है कि इन लक्षणों की के लिए योगात्मक आनुवंशिक नियंत्रण की प्राबल्यता पाई गई। बीस जीनोटाइप को D² विश्लेषण के आधार पर तीन समूह में बांटा गया। प्रथम समूह में तीन जीनोटाइप को शामिल किया गया जो कि प्राथमिक शाखाओं की संख्या एवं द्वितीय शाखाओं की संख्या प्रति पादप के लिए उच्च समूह माध्य दर्शाता है। द्वितीय समूह में सोलह जीनोटाइप शामिल हुए एवं समूह ने पौधे की ऊँचाई, कॉलर व्यास और फूल आने के दिनों की संख्या के लिए उच्च समूह माध्य मुल्यता दर्शाई। एक जीनोटाइप तृतीय समूह का प्रतिनिधित्व करते हुए फूल अवधि के बाद के दिनों की संख्या एवं फल प्रति समूह के लिए उच्च समूह माध्य दर्ज की। अधिकतम अंतर-समूह की दूरी, समूह द्वितीय एवं तृतीय के बीच पाई गई और न्यूनतम अंतर-समूह दूरी प्रथम एवं द्वितीय समूह के बीच पाई गई जबकि प्रथम समूह, द्वितीय एवं तृतीय समूह से समान दूरी पर पाया गया। प्रायोगिक परिणामों से ज्ञात होता है कि बीज उपज प्रति पादप, फल प्रति समूह एवं फूल अवधि के बाद के दिनों की संख्या ने आनुवांशिक विविधता में अधिकतम योगदान दिया और आनुवंशिक विविधता जेट्रोफा जीनोटाइप की भौगोलिक विविधता के साथ संयोजित नहीं पाई गई। अतः उच्च आनुवांशिक विविधता की क्षमता रखने वाले जीनोटाइप जैसे कि, आई. जी. ए. यू. रायपुर, आई. जी. ए. यू. सरगुजा एवं टी एन एम सी.- तीन को जेट्रोफा बीज उत्पादकता की वृद्धि के लिए आनुवंशिक संघटन को सुधारने में जनक के रूप में प्रयोग किया जा सकता है।


(बी.बी. बन्धोपाध्याय)
सलाहकार


(सुभाष चन्द)
लेखक